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(54) Title: METHOD FOR MODIFYING PLANT BIOMASS

(57) Abstract: Recombinant polynucleotides and methods for modifying the phenotype of a plant are provided. In preferred embodiments, the phenotype modified is a plant's biomass. Modifying plant biomass leads to improved yields for leafy crops, for example. The method comprises altering the levels of a transcription factor that is introduced into the plant or that is endogenous to the plant to obtain a plant with a larger biomass.

METHOD FOR MODIFYING PLANT BIOMASS

This application claims priority to U.S. Patent Application Serial No. 09/823,676, filed March 30, 2001.

FIELD OF THE INVENTION

This invention relates to the field of plant biology. More particularly, the present invention pertains to compositions and methods for phenotypically modifying a plant.

BACKGROUND OF THE INVENTION

Increasing the biomass of a plant has several commercial applications. For example, increasing plant leaf biomass may increase the yield of leafy vegetables for human or animal consumption. Additionally, increasing leaf biomass can be used to increase production of plant-derived pharmaceutical or industrial products. By increasing plant biomass, increased production levels of the products may be obtained from the plants. Tobacco leaves, in particular, have been employed as plant factories to generate such products. Furthermore, it may be desirable to increase crop yields of plants by increasing total plant photosynthesis. An increase in total plant photosynthesis is typically achieved by increasing leaf area of the plant. Additional photosynthetic capacity may be used to increase the yield derived from particular plant tissue, including the leaves, roots, fruits or seed. In addition, the ability to modify the biomass of the leaves may be useful for permitting the growth of a plant under decreased light intensity or under high light intensity. Modification of the biomass of another tissue, such as roots, may be useful to improve a plant's ability to grow under harsh environmental conditions, including drought or nutrient deprivation, because the roots may grow deeper into the ground.

Thus, the present invention provides a method for modifying the plant biomass by modifying the size or number of leaves or seed of a plant.

SUMMARY OF THE INVENTION

In a first aspect, the invention relates to a recombinant polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) a nucleotide sequence encoding a polypeptide comprising a sequence selected from SEQ ID NO: 2, 4, 6, and 8, or a complementary nucleotide sequence thereof; (b) a nucleotide sequence encoding a polypeptide comprising a conservatively substituted variant of a polypeptide of (a); (c) a nucleotide sequence comprising a sequence selected from those of SEQ ID NO: 1, 3, 5 and 7, or a complementary nucleotide sequence thereof; (d) a nucleotide sequence comprising silent substitutions in a nucleotide sequence of (c); (e) a nucleotide sequence which hybridizes under stringent conditions over substantially the entire length of a nucleotide sequence of one or more of: (a), (b), (c), or (d); (f) a nucleotide sequence comprising at least 15 consecutive nucleotides of a sequence of any of (a)-(e); (g) a nucleotide sequence comprising a subsequence or fragment of any of (a)-(f), which subsequence or fragment encodes a polypeptide having a biological activity that modifies a plant's biomass; (h) a nucleotide sequence having at least 40% sequence identity to a nucleotide sequence of any of (a)-(g); (i) a nucleotide sequence having at least 85% sequence identity to a nucleotide sequence of any of (a)-(g); (j) a nucleotide sequence which encodes a polypeptide having at least 40% sequence identity to a polypeptide of SEQ ID NO: 2, 4, 6 or 8; (k) a nucleotide sequence which encodes a polypeptide having at least 85% identity sequence identity to a polypeptide of SEQ ID NO: 2, 4, 6 or 8; (l) a nucleotide sequence which encodes a conserved domain of a polypeptide having at least 65% sequence identity to a conserved domain of a polypeptide of SEQ ID NO: 2, 4, 6, or 8; (m) a nucleotide sequence which encodes a plant transcription factor comprising a fragment having 6 consecutive amino acids from a region of SEQ ID NO: 2, 4, 6, or 8 outside of the conserved domain; (n) a nucleotide sequence having at least 85% sequence identity to (m); (o) a nucleotide sequence which encodes a plant transcription factor comprising a fragment having 8 consecutive amino acids from a region of SEQ ID NO: 2, 4, 6, or 8 outside of the conserved domain; and (p) a nucleotide sequence having at least 85% sequence identity to (o). Homologous sequences, paralogs, orthologs and/or homologs as described herein or recited in the Tables are also specifically included in the polynucleotides and polypeptides of the

invention. The recombinant polynucleotide may further comprise a constitutive, inducible, or tissue-specific promoter operably linked to the nucleotide sequence. The invention also relates to compositions comprising at least two of the above described polynucleotides.

In a second aspect, the invention is an isolated or recombinant polypeptide comprising a subsequence of at least about 15 contiguous amino acids encoded by the recombinant or isolated polynucleotide described above. These polynucleotides and polypeptides are useful for modifying plant biomass, either by increasing or decreasing the size of the leaves, the roots, the flowers, the seeds, the stalk or the like.

In another aspect, the invention is a transgenic plant comprising one or more of the above described recombinant polynucleotides. In yet another aspect, the invention is a plant with altered expression levels of a polynucleotide described above or a plant with altered expression or activity levels of an above described polypeptide. In a further aspect, the invention relates to a cloning or expression vector comprising the isolated or recombinant polynucleotide described above or cells comprising the cloning or expression vector.

In yet a further aspect, the invention relates to a composition produced by incubating a polynucleotide of the invention with a nuclease, a restriction enzyme, a polymerase; a polymerase and a primer; a cloning vector, or with a cell.

Furthermore, the invention relates to a method for producing a plant having a modified plant biomass. The method comprises altering the expression of an isolated or recombinant polynucleotide of the invention or altering the expression or activity of a polypeptide of the invention in a plant to produce a modified plant, and selecting the modified plant for increased or decreased biomass.

In another aspect, the invention relates to a method of identifying a factor that is modulated by or interacts with a polypeptide encoded by a polynucleotide of the invention. The method comprises expressing a polypeptide encoded by the polynucleotide in a plant and identifying at least one factor that is modulated by or interacts with the polypeptide. In one embodiment the method for identifying modulating or interacting factors is by detecting binding by the polypeptide to a promoter sequence, or by detecting interactions between an

additional protein and the polypeptide in a yeast two hybrid system, or by detecting expression of a factor by hybridization to a microarray, subtractive hybridization or differential display.

In yet another aspect, the invention is a method of identifying a molecule that modulates activity or expression of a polynucleotide or polypeptide of interest. The method comprises placing the molecule in contact with a plant comprising the polynucleotide or polypeptide encoded by the polynucleotide of the invention and monitoring one or more of the expression level of the polynucleotide in the plant, the expression level of the polypeptide in the plant, and modulation of an activity of the polypeptide in the plant.

In yet another aspect, the invention relates to an integrated system, computer or computer readable medium comprising one or more character strings corresponding to a polynucleotide of the invention, or to a polypeptide encoded by the polynucleotide. The integrated system, computer or computer readable medium may comprise a link between one or more sequence strings to a modified biomass phenotype.

In yet another aspect, the invention is a method for identifying a sequence similar or homologous to one or more polynucleotides of the invention, or one or more polypeptides encoded by the polynucleotides. The method comprises providing a sequence database and querying the sequence database with one or more target sequences corresponding to the one or more polynucleotides or to the one or more polypeptides to identify one or more sequence members of the database that display sequence similarity or homology to one or more of the target sequences.

BRIEF DESCRIPTION OF THE SEQUENCE LISTING AND DRAWINGS

The Sequence Listing provides exemplary polynucleotide and polypeptide sequences of the invention. These sequences may be employed to modify the biomass of a plant.

Figure 1 shows the polypeptide alignments for G1073 (SEQ ID Nos. 1 and 2), G2789 (SEQ ID Nos. 3 and 4), G1945 (SEQ ID Nos. 5 and 6) and G2155 (SEQ ID Nos. 7 and 8) showing regions of the polypeptides with sequence identity.

Figure 2 shows that plants overexpressing G1073 have an increased fresh weight, dry weight and seed yield (greater than 150%) when compared with plants that do not overexpress G1073.

Figure 3 contains photographs of a plant overexpressing G1073 and a wild-type plant (wt) and demonstrates that plants overexpressing G1073 have an increased biomass when compared with control or reference plants.

DETAILED DESCRIPTION

Each of the references, documents or information sources listed herein is specifically incorporated into this application and can be relied on to make or use the invention.

The present invention relates to polynucleotides and polypeptides, e.g. for modifying phenotypes of plants. In particular, the polynucleotides or polypeptides are useful for modifying plant biomass when the expression levels of the polynucleotides or expression levels or activity levels of the polypeptides are altered compared with those found in a wild type plant. Plant biomass can be either decreased, increased or made inducible under specific conditions using the polynucleotides or polypeptides of this invention.

The polynucleotides of the invention encode plant transcription factors. The plant transcription factors are derived, e.g., from *Arabidopsis thaliana* and can belong, e.g., to one or more of the following transcription factor families: the AP2 (APETALA2) domain transcription factor family (Riechmann and Meyerowitz (1998) Biol. Chem. 379:633-646); the MYB transcription factor family (Martin and Paz-Ares (1997) Trends Genet. 13:67-73); the MADS domain transcription factor family (Riechmann and Meyerowitz (1997) Biol. Chem. 378:1079-1101); the WRKY protein family (Ishiguro and Nakamura (1994) Mol. Gen. Genet. 244:563-571); the ankyrin-repeat protein family (Zhang et al. (1992) Plant Cell 4:1575-1588); the miscellaneous protein (MISC) family (Kim et al. (1997) Plant J. 11:1237-1251); the zinc finger protein (Z) family (Klug and Schwabe (1995) FASEB J. *9:* 597-604); the homeobox (HB) protein family (Buerglin in Duboule (1994) Guidebook to the Homeobox Genes, Oxford University Press); the CAAT-element binding proteins (Forsburg and Guarente (1989) Genes Dev. 3:1166-1178); the squamosa promoter binding proteins

(SPB) (Klein et al. (1996) Mol. Gen. Genet. 1996 250:7-16); the NAM protein family; the IAA/AUX proteins (Rouse et al. (1998) Science 279:1371–1373); the HLH/MYC protein family (Littlewood et al. (1994) Prot. Profile 1:639-709); the DNA-binding protein (DBP) family (Tucker et al. (1994) EMBO J. 13:2994-3002); the bZIP family of transcription factors (Foster et al. (1994) FASEB J. 8:192-200); the BPF-1 protein (Box P-binding factor) family (da Costa e Silva et al. (1993) Plant J. 4:125-135); the golden protein (GLD) family (Hall et al. (1998) Plant Cell 10:925-936); and the AT-hook protein (AT-Hook) family (Aravind et al. (1998) Nucl. Acid Res. 26: 4413-4421). Exemplary transcription factors of the present invention are listed in the Sequence Listing.

In addition to methods for modifying a plant phenotype by employing one or more polynucleotides and polypeptides of the invention described herein, the polynucleotides and polypeptides of the invention have a variety of additional uses. These uses include their use in the recombinant production (i.e, expression) of proteins, as regulators of plant gene expression, as diagnostic probes for the presence of complementary or partially complementary nucleic acids (including for detection of natural coding nucleic acids), as substrates for further reactions, e.g., mutation reactions, PCR reactions, or the like, or as substrates for cloning e.g., including digestion or ligation reactions, and for identifying exogenous or endogenous modulators of the transcription factors.

DEFINITIONS

A "polynucleotide" is a nucleic acid sequence comprising a plurality of polymerized nucleotide residues, e.g., at least about 15 consecutive polymerized nucleotide residues, optionally at least about 30 consecutive nucleotides, or at least about 50 consecutive nucleotides. In many instances, a polynucleotide comprises a nucleotide sequence encoding a polypeptide (or protein) or a domain or fragment thereof. Additionally, the polynucleotide may comprise a promoter, an intron, an enhancer region, a polyadenylation site, a translation initiation site, 5' or 3' untranslated regions, a reporter gene, a selectable marker, a purification tag, or the like. The polynucleotide can be single stranded or double stranded DNA or RNA. The polynucleotide optionally comprises modified bases or a modified backbone.

The polynucleotide can be, e.g., genomic DNA or RNA, a transcript (such as an mRNA), a cDNA, a PCR product, a cloned DNA, a synthetic DNA or RNA, or the like. The polynucleotide can comprise a sequence in either sense or antisense orientations.

A "recombinant polynucleotide" is a polynucleotide that is not in its native state, e.g., the polynucleotide comprises a nucleotide sequence not found in nature, or the polynucleotide is in a context other than that in which it is naturally found, e.g., separated from nucleotide sequences with which it typically is in proximity in nature, or adjacent (or contiguous with) nucleotide sequences with which it typically is not in proximity. For example, the sequence at issue can be cloned into a vector, or otherwise recombined with one or more additional nucleic acid.

An "isolated polynucleotide" is a polynucleotide whether naturally occurring or recombinant, that is present outside the cell in which it is typically found in nature, whether purified or not. Optionally, an isolated polynucleotide is subject to one or more enrichment or purification procedures, e.g., cell lysis, extraction, centrifugation, precipitation, or the like.

A "recombinant polypeptide" is a polypeptide produced by translation of a recombinant polynucleotide. An "isolated polypeptide," whether a naturally occurring or a recombinant polypeptide, is more enriched in (or out of) a cell than the polypeptide in its natural state in a wild type cell, e.g., more than about 5% enriched, more than about 10% enriched, or more than about 20%, or more than about 50%, or more, enriched, i.e., alternatively denoted: 105%, 110%, 120%, 150%, 300% or more, enriched relative to wild type standardized at 100%. Such an enrichment is not the result of a natural response of a wild type plant. Alternatively, or additionally, the isolated polypeptide is separated from other cellular components with which it is typically associated, e.g., by any of the various protein purification methods herein.

The term "transgenic plant" refers to a plant that contains genetic material, not found in a wild type plant of the same species, variety or cultivar. The genetic material may include a transgene, an insertional mutagenesis event (such as by transposon or T-DNA insertional mutagenesis), an activation tagging sequence, a mutated sequence, a homologous recombination event or a sequence modified by

chimeraplasty. Typically, the foreign genetic material has been introduced into the plant by human manipulation.

A transgenic plant may contain an expression vector or cassette. The expression cassette typically comprises a polypeptide-encoding sequence operably linked (i.e., under regulatory control of) to appropriate inducible or constitutive regulatory sequences that allow for the expression of polypeptide. The expression cassette can be introduced into a plant by transformation or by breeding after transformation of a parent plant. A plant refers to a whole plant as well as to a plant part, such as seed, fruit, leaf, or root, plant tissue, plant cells or any other plant material, e.g., a plant explant, as well as to progeny thereof, and to *in vitro* systems that mimic biochemical or cellular components or processes in a cell.

The phrase "ectopically expression or altered expression" in reference to a polynucleotide indicates that the pattern of expression in, e.g., a transgenic plant or plant tissue, is different from the expression pattern in a wild type plant or a reference plant of the same species. For example, the polynucleotide or polypeptide is expressed in a cell or tissue type other than a cell or tissue type in which the sequence is expressed in the wild type plant, or by expression at a time other than at the time the sequence is expressed in the wild type plant, or by a response to different inducible agents, such as hormones or environmental signals, or at different expression levels (either higher or lower) compared with those found in a wild type plant. The term also refers to altered expression patterns that are produced by lowering the levels of expression to below the detection level or completely abolishing expression. The resulting expression pattern can be transient or stable, constitutive or inducible. In reference to a polypeptide, the term "ectopic expression or altered expression" may further relate to altered activity levels resulting from the interactions of the polypeptides with exogenous or endogenous modulators or from interactions with factors or as a result of the chemical modification of the polypeptides.

The term "fragment" or "domain," with respect to a polypeptide, refers to a subsequence of the polypeptide. In some cases, the fragment or domain is a subsequence of the polypeptide, which performs at least one biological function of the intact polypeptide in substantially the same manner, or to a similar extent, as does the

intact polypeptide. For example, a polypeptide fragment can comprise a recognizable structural motif or functional domain such as a DNA binding domain that binds to a DNA promoter region, an activation domain or a domain for protein-protein interactions. Fragments can vary in size from as few as 5, 6 or 8 amino acids to the full length of the intact polypeptide, but are preferably at least about 30 amino acids in length and more preferably at least about 60 amino acids in length. In reference to a nucleotide sequence, “a fragment” refers to any subsequence of a polynucleotide, typically, of at least consecutive about 15 nucleotides, encoding 5, 6, 8 or 10 amino acids for example, preferably at least about 30 nucleotides, more preferably at least about 50, of any of the sequences provided herein. A fragment can consist of or comprise nucleotides encoding amino acids outside of a conserved domain known to exist in a particular transcription factor belonging to a transcription factor family, for example.

The term “trait” refers to a physiological, morphological, biochemical or physical characteristic of a plant or particular plant material or cell. In some instances, this characteristic is visible to the human eye, such as seed or plant size, or can be measured by available biochemical techniques, such as the protein, starch or oil content of seed or leaves or by the observation of the expression level of genes, e.g., by employing Northern analysis, RT-PCR, microarray gene expression assays or reporter gene expression systems, or by agricultural observations such as stress tolerance, yield or pathogen tolerance.

“Trait modification” refers to a detectable difference in a characteristic in a plant ectopically expressing a polynucleotide or polypeptide of the present invention relative to a plant not doing so, such as a wild type plant. In some cases, the trait modification can be evaluated quantitatively. For example, the trait modification can entail at least about a 2% increase or decrease in an observed trait (difference), at least about a 5% difference, at least about a 10% difference, at least about a 20% difference, at least about a 30%, at least about a 50%, at least about a 70%, or at least about a 100%, at least a 300% or an even greater difference. It is known that there can be a natural variation in the modified trait. Therefore, the trait modification observed entails a change of the normal distribution of the trait in the plants compared with the distribution observed in wild type plant.

POLYPEPTIDES AND POLYNUCLEOTIDES OF THE INVENTION

The present invention provides, among other things, transcription factors (TFs), and transcription factor homologue polypeptides, and isolated or recombinant polynucleotides encoding the polypeptides. These polypeptides and polynucleotides may be employed to modify a plant's biomass.

Exemplary polynucleotides encoding the polypeptides of the invention were identified in the *Arabidopsis thaliana* GenBank database using publicly available sequence analysis programs and parameters. Sequences initially identified were then further characterized to identify sequences comprising specified sequence strings corresponding to sequence motifs present in families of known transcription factors. Polynucleotide sequences meeting such criteria were confirmed as transcription factors.

Additional polynucleotides of the invention were identified by screening *Arabidopsis thaliana* and/or other plant cDNA libraries with probes corresponding to known transcription factors under low stringency hybridization conditions. Additional sequences, including full length coding sequences were subsequently recovered by the rapid amplification of cDNA ends (RACE) procedure, using a commercially available kit according to the manufacturer's instructions. Where necessary, multiple rounds of RACE are performed to isolate 5′ and 3′ ends. The full length cDNA was then recovered by a routine end-to-end polymerase chain reaction (PCR) using primers specific to the isolated 5′ and 3′ ends. Exemplary sequences are provided in the Sequence Listing.

The polynucleotides of the invention were ectopically expressed in overexpressor or knockout plants and changes in plant biomass were observed. Therefore, the polynucleotides and polypeptides can be employed to improve (increase or decrease) plant biomass.

Making polynucleotides

The polynucleotides of the invention include sequences that encode transcription factors and transcription factor homologue polypeptides and sequences complementary thereto, as well as unique fragments of coding sequence, or sequence complementary thereto. Such polynucleotides can be, e.g., DNA or RNA, mRNA,

cRNA, synthetic RNA, genomic DNA, cDNA synthetic DNA, oligonucleotides, etc. The polynucleotides are either double-stranded or single-stranded, and include either, or both sense (i.e., coding) sequences and antisense (i.e., non-coding, complementary) sequences. The polynucleotides include the coding sequence of a transcription factor, or transcription factor homologue polypeptide, in isolation, in combination with additional coding sequences (e.g., a purification tag, a localization signal, as a fusion-protein, as a pre-protein, or the like), in combination with non-coding sequences (e.g., introns or inteins, regulatory elements such as promoters, enhancers, terminators, and the like), and/or in a vector or host environment in which the polynucleotide encoding a transcription factor or transcription factor homologue polypeptide is an endogenous or exogenous gene.

A variety of methods exist for producing the polynucleotides of the invention. Procedures for identifying and isolating DNA clones are well known to those of skill in the art, and are described in, e.g., Berger and Kimmel, Guide to Molecular Cloning Techniques, Methods in Enzymology volume 152 Academic Press, Inc., San Diego, CA ("Berger"); Sambrook et al., Molecular Cloning - A Laboratory Manual (2nd Ed.), Vol. 1-3, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, 1989 ("Sambrook") and Current Protocols in Molecular Biology, F.M. Ausubel et al., eds., Current Protocols, a joint venture between Greene Publishing Associates, Inc. and John Wiley & Sons, Inc., (supplemented through 2000) ("Ausubel").

Alternatively, polynucleotides of the invention can be produced by a variety of in vitro amplification methods adapted to the present invention by appropriate selection of specific or degenerate primers. Examples of protocols sufficient to direct persons of skill through in vitro amplification methods, including the polymerase chain reaction (PCR) the ligase chain reaction (LCR), Qbeta-replicase amplification and other RNA polymerase mediated techniques (e.g., NASBA), e.g., for the production of the homologous nucleic acids of the invention are found in Berger, Sambrook, and Ausubel, as well as Mullis et al., (1987) PCR Protocols A Guide to Methods and Applications (Innis et al. eds) Academic Press Inc. San Diego, CA (1990) (Innis). Improved methods for cloning in vitro amplified nucleic acids are described in Wallace et al., U.S. Pat. No. 5,426,039. Improved methods for

amplifying large nucleic acids by PCR are summarized in Cheng et al. (1994) Nature 369: 684-685 and the references cited therein, in which PCR amplicons of up to 40kb are generated. One of skill will appreciate that essentially any RNA can be converted into a double stranded DNA suitable for restriction digestion, PCR expansion and sequencing using reverse transcriptase and a polymerase. See, e.g., Ausubel, Sambrook and Berger, all *supra.*

Alternatively, polynucleotides and oligonucleotides of the invention can be assembled from fragments produced by solid-phase synthesis methods. Typically, fragments of up to approximately 100 bases are individually synthesized and then enzymatically or chemically ligated to produce a desired sequence, e.g., a polynucleotide encoding all or part of a transcription factor. For example, chemical synthesis using the phosphoramidite method is described, e.g., by Beaucage et al. (1981) Tetrahedron Letters 22:1859-69; and Matthes et al. (1984) EMBO J. 3:801-5. According to such methods, oligonucleotides are synthesized, purified, annealed to their complementary strand, ligated and then optionally cloned into suitable vectors. And if so desired, the polynucleotides and polypeptides of the invention can be custom ordered from any of a number of commercial suppliers.

HOMOLOGOUS SEQUENCES

Sequences homologous, i.e., that share significant sequence identity or similarity, to those provided in the Sequence Listing, derived from *Arabidopsis thaliana* or from other plants of choice are also an aspect of the invention. Homologous sequences can be derived from any plant including monocots and dicots and in particular agriculturally important plant species including, but not limited to, crops such as soybean, wheat, corn, potato, cotton, rice, oilseed rape (including canola), sunflower, alfalfa, sugarcane and turf; or fruits and vegetables, such as banana, blackberry, blueberry, strawberry, and raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honeydew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits (such as apple, peach, pear, cherry and plum) and vegetable brassicas (such as broccoli, cabbage, cauliflower, brussel sprouts and kohlrabi). Other crops, fruits and vegetables whose phenotype can be changed

include barley, rye, millet, sorghum, currant, avocado, citrus fruits such as oranges, lemons, grapefruit and tangerines, artichoke, cherries, nuts such as the walnut and peanut, endive, leek, roots, such as arrowroot, beet, cassava, turnip, radish, yam, and sweet potato, and beans. The homologous sequences may also be derived from woody species, such pine, poplar and eucalyptus.

Transcription factors that are homologous to the listed sequences will typically share at least about 35% amino acid sequence identity. More closely related transcription factors can share at least about 50%, about 60%, about 65%, about 70%, about 75% or about 80% or about 90% or about 95% or about 98% or more sequence identity with the listed sequences. Factors that are most closely related to the listed sequences share, e.g., at least about 85%, about 90% or about 95% or more sequence identity to the listed sequences. At the nucleotide level, the sequences will typically share at least about 40% nucleotide sequence identity, preferably at least about 50%, about 60%, about 70% or about 80% sequence identity, and more preferably about 85%, about 90%, about 95% or about 97% or more sequence identity to one or more of the listed sequences. The degeneracy of the genetic code enables major variations in the nucleotide sequence of a polynucleotide while maintaining the amino acid sequence of the encoded protein. Conserved domains within a transcription factor family may exhibit a higher degree of sequence homology, such as at least 65% sequence identity including conservative substitutions, and preferably at least 80% sequence identity. Exemplary conserved domains of the present invention include for example, for G1073 (SEQ ID NO: 1 and 2) amino acid residues 35 through 40 or 42 through 48 which are conserved in each of the sequences G2789 (SEQ ID NO: 3 and 4), G1945 (SEQ ID NO: 5 and 6) and G2155 (SEQ ID NO: 7 and 8). Transcription factors of the invention can also contain 5, 6, 8, 10 or 12 consecutive amino acids from the sequences of SEQ ID NO: 2, 4, 6 or 8 where the consecutive amino acids are taken from a region outside of the conserved domain. Polynucleotides having at least 90%, or at least 85%, or at least 75%, or at least 60%, or at least 50%, or at least 40% sequence identity to those encoding the above transcription factors are also included in this invention.

Orthologs and Paralogs

Several different methods are known by those of skill in the art for identifying and defining these functionally homologous sequences. Three general methods for defining paralogs and orthologs are described; a paralog or ortholog may be identified by only one or more of the methods described below.

Orthologs and paralogs are evolutionarily related genes that have similar sequences and similar functions. Paralogs are related genes within a single species and are most likely a result of gene duplication, whereas orthologs are related genes in different species derived from a common ancestral molecule prior to speciation.

Within a single plant species, gene duplication may cause two copies of a particular gene, giving rise to two or more genes with similar sequence and similar function known as paralogs. A paralog is therefore a similar gene with a similar function within the same species. Paralogs typically cluster together or in the same clade (a group of similar genes), as is shown when a gene family phylogeny is analyzed using programs such as CLUSTAL (Thompson et al. (1994) Nucleic Acids Res. 22:4673-4680; Higgins et al. (1996) Methods Enzymol. 266 383-402). Groups of similar genes can also be identified using by pair-wise BLAST analysis (Feng and Doolittle (1987) J. Mol. Evol. 25:351-360). For example, a clade of very similar MADS domain transcription factors from Arabidopsis all share a common function in flowering time (Ratcliffe et al. (2001) Plant Physiol. 126:122-132), and a group of very similar AP2 domain transcription factors from Arabidopsis are involved in tolerance of plants to freezing (Gilmour et al. (1998) Plant J. 16:433-442). Analysis of groups of similar genes with similar function that fall within one clade can yield subsequences that are particular to the clade. These subsequences, known as consensus sequences, can not only be used to define the sequences within each clade, but define the functions of these genes, since genes within each clade typically share the same function. (See also, for example, Mount, D.W. (2001) Bioinformatics: Sequence and Genome Analysis Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York page 543.)

Speciation, the production of new species from a parental species, can also give rise to two or more genes with similar sequence and similar function. These

genes, termed orthologs, often have an identical function within their host plants and are often interchangeable between species without losing function. Because plants have common ancestors, many genes in any plant species will have a corresponding orthologous gene in another plant species. Once a phylogenic tree for a gene family of one species has been constructed using a program such as CLUSTAL (Thompson et al. (1994) Nucleic Acids Res. 22:4673-4680; Higgins et al. (1996) Methods Enzymol. 266:383-402), potential orthologous sequences can placed into the phylogenetic tree and their relationship to genes from the species of interest can be determined. Once the ortholog pair has been identified, the function of the test ortholog can be determined by determining the function of the reference ortholog.

Orthologs can also be identified by pair-wise BLAST analysis by aligning a set of reference sequences against a set of test sequences. Test sequences with the closest match to a particular reference sequence, as determined by the P-value of the BLAST analysis, can be taken and individually aligned against the reference set of sequences. The individual test sequence will either best match the particular reference sequence, in which case it is likely to be an ortholog, or not, in which case it may not be an ortholog.

A further way of identifying an ortholog is by identifying a consensus sequence within the candidate ortholog. Using pair-wise BLAST analysis, or programs such as CLUSTAL alignment program, sets of similar genes, or clades, can be identified. The particular subsequences that define commonalities within a particular clade can be derived from an alignment of those sequences. Orthologs would have the consensus sequence, or a sequence similar to the consensus sequence. Orthologs might also have a consensus sequence outside a conserved domain, which could be particular to that family of orthologous sequences.

Corresponding orthologs may bridge the monocot/dicot division of the plant kingdom and orthologous pairs of genes can be identified in rice and Arabidopsis, corn and Arabidopsis and Antirhinnum and corn. For example Peng et al showed that a mutant of the *Arabidopsis* gene termed *Gibberellin Insensitive* (*GAI;* mutant termed *gai*) encoded a transcription factor and which conferred a reduction in gibberellin responsiveness in the native plant (Peng et al. 1997 Genes and Development 11:3194-3205). In addition, Peng et al. subsequently showed that the

Arabidopsis GAI protein has 62 % amino acid residue identity with the wheat Rht-D1a protein and 62 % amino acid residue identity with the maize d8. Peng et al. showed that transgenic rice plants containing a mutant GAI allele give reduced response to gibberellin and are dwarfed, mimicking the dwarfed wheat variety from which the mutant *Rht-D1a* gene was isolated. Peng et al. taught that Arabidopsis GAI protein is an ortholog of the wheat Rht-D1a and maize d8 proteins. (Peng et al. 1999 Nature 400:256-261.)

In addition Fu et al. (2001 Plant Cell 13:1791-1802), Nandi et al. (2000 Curr. Biol. 10:215-218), Coupland (1995 Nature 377:482-483), and Weigel and Nilsson (1995 Nature 377:482-500) show that an Arabidopsis transcription factor expressed in an exogenous plant species elicits the same or very similar phenotypic response. Furthermore, Kater et al. (1998 Plant Cell 10:171-182), Mandel et al. (1992 Cell 71-133-143), and Suzuki et al. (2001 Plant J. 28:409-418) showed that a transcription factor expressed in another plant species elicits the same or very similar phenotypic response of the endogenous sequence, as often predicted in earlier studies of Arabidopsis transcription factors in Arabidopsis.

Table 1 (appended to this application) lists a summary of orthologous and homologous sequences identified using BLAST (tblastx program) and the standard BLAST result data generated from a search. The first column shows the polynucleotide sequence identifier (SEQ ID NO), the second column shows the transcription factor cDNA identifier (Gene ID), the third column shows the GenBank Accession Number of the orthologous or homologous polynucleotide sequence identified in a BLAST search (Test Sequence ID), the fourth column shows the calculated probability value that the sequence identity is due to chance (Smallest Sum Probability), the fifth column identifies the plant species of the Test Sequence (Test Sequence Species), and the sixth column shows the GenBank annotation for the sequence identified in a BLAST search (Test Sequence GenBank Annotation).

Table 2 (appended to this application) lists orthologous and homologous sequences identified using BLAST (tblastx program) and the standard BLAST result data generated from a search. The first column shows the polynucleotide sequence identifier (SEQ ID NO), the second column shows the transcription factor cDNA identifier (Gene ID), the third column shows the GenBank

Accession Number of the orthologous or homologous polynucleotide (Test Sequence ID), the fourth column shows the GenBank annotation for the sequence identified in a BLAST search (Test Sequence GenBank Annotation), the fifth column shows the reading frame of the Test sequence encoding the orthologous or homologous sequence (Reading Frame), the sixth column shows the calculated score value of the aligned sequences (High Score), the seventh column shows the calculated probability value that the sequence identity is due to chance (Smallest Sum Probability), and the eighth column shows the number of regions in the Test Sequence that align with a sequence from the SEQ ID NO. (N).

Identifying Nucleic Acids by Hybridization

Polynucleotides homologous to the sequences illustrated in the Sequence Listing can be identified in a variety of ways known to one skilled in the art, e.g., by hybridization to each other under stringent or under highly stringent conditions. Single stranded polynucleotides hybridize when they associate based on a variety of well characterized physico-chemical forces, such as hydrogen bonding, solvent exclusion, base stacking and the like. The stringency of a hybridization reflects the degree of sequence identity of the nucleic acids involved, such that the higher the stringency, the more similar are the two polynucleotide strands. Stringency is influenced by a variety of factors, including temperature, salt concentration and composition, organic and non-organic additives, solvents, etc. present in both the hybridization and wash solutions and incubations (and number), as described in more detail in the references cited above.

An example of stringent hybridization conditions for hybridization of complementary nucleic acids which have more than 100 complementary residues on a filter in a Southern or northern blot is about 5°C to 20°C lower than the thermal melting point (Tm) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Nucleic acid molecules that hybridize under stringent conditions will typically hybridize to a probe based on either the entire cDNA or selected portions, e.g., to a unique subsequence, of the cDNA under wash conditions of 0.2x SSC to 2.0 x SSC, 0.1% SDS at 50-65° C, for example

0.2 x SSC, 0.1% SDS at 65° C. For identification of less closely related homologues washes can be performed at a lower temperature, e.g., 50° C. In general, stringency is increased by raising the wash temperature and/or decreasing the concentration of SSC.

As another example, stringent conditions can be selected such that an oligonucleotide that is perfectly complementary to the coding oligonucleotide hybridizes to the coding oligonucleotide with at least about a 5-10x higher signal to noise ratio than the ratio for hybridization of the perfectly complementary oligonucleotide to a nucleic acid encoding a transcription factor known as of the filing date of the application. Conditions can be selected such that a higher signal to noise ratio is observed in the particular assay which is used, e.g., about 15x, 25x, 35x, 50x or more. Accordingly, the subject nucleic acid hybridizes to the unique coding oligonucleotide with at least a 2x higher signal to noise ratio as compared to hybridization of the coding oligonucleotide to a nucleic acid encoding known polypeptide. Again, higher signal to noise ratios can be selected, e.g., about 5x, 10x, 25x, 35x, 50x or more. The particular signal will depend on the label used in the relevant assay, e.g., a fluorescent label, a colorimetric label, a radioactive label, or the like.

Alternatively, transcription factor homologue polypeptides can be obtained by screening an expression library using antibodies specific for one or more transcription factors. With the disclosed transcription factor and transcription factor homologue nucleic acid sequences, the encoded polypeptide(s) can be expressed and purified in a heterologous expression system (e.g., *E. coli*) and used to raise antibodies (monoclonal or polyclonal) specific for the polypeptide(s) in question. Antibodies can also be raised against synthetic peptides derived from transcription factor, or transcription factor homologue, amino acid sequences. Methods of raising antibodies are well known in the art and are described in Harlow and Lane (1988) Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory, New York. Such antibodies can then be used to screen an expression library produced from the plant from which it is desired to clone additional transcription factor homologues, using the

methods described above. The selected cDNAs can be confirmed by sequencing and enzymatic activity.

SEQUENCE VARIATIONS

It will readily be appreciated by those of skill in the art, that any of a variety of polynucleotide sequences are capable of encoding the transcription factors and transcription factor homologue polypeptides of the invention. Due to the degeneracy of the genetic code, many different polynucleotides can encode identical and/or substantially similar polypeptides in addition to those sequences illustrated in the Sequence Listing.

For example, Table 3 illustrates, e.g., that the codons AGC, AGT, TCA, TCC, TCG, and TCT all encode the same amino acid: serine. Accordingly, at each position in the sequence where there is a codon encoding serine, any of the above trinucleotide sequences can be used without altering the encoded polypeptide.

Table 3

Amino acids			Codon					
Alanine	Ala	A	GCA	GCC	GCG	GCU		
Cysteine	Cys	C	TGC	TGT				
Aspartic acid	Asp	D	GAC	GAT				
Glutamic acid	Glu	E	GAA	GAG				
Phenylalanine	Phe	F	TTC	TTT				
Glycine	Gly	G	GGA	GGC	GGG	GGT		
Histidine	His	H	CAC	CAT				
Isoleucine	Ile	I	ATA	ATC	ATT			
Lysine	Lys	K	AAA	AAG				
Leucine	Leu	L	TTA	TTG	CTA	CTC	CTG	CTT
Methionine	Met	M	ATG					
Asparagine	Asn	N	AAC	AAT				
Proline	Pro	P	CCA	CCC	CCG	CCT		
Glutamine	Gln	Q	CAA	CAG				
Arginine	Arg	R	AGA	AGG	CGA	CGC	CGG	CGT
Serine	Ser	S	AGC	AGT	TCA	TCC	TCG	TCT
Threonine	Thr	T	ACA	ACC	ACG	ACT		
Valine	Val	V	GTA	GTC	GTG	GTT		
Tryptophan	Trp	W	TGG					
Tyrosine	Tyr	Y	TAC	TAT				

Sequence alterations that do not change the amino acid sequence encoded by the polynucleotide are termed "silent" variations. With the exception of the codons ATG and TGG, encoding methionine and tryptophan, respectively, any of the possible codons for the same amino acid can be substituted by a variety of techniques, e.g., site-directed mutagenesis, available in the art. Accordingly, any and all such variations of a sequence selected from the above table are a feature of the invention.

In addition to silent variations, other conservative variations that alter one, or a few amino acids in the encoded polypeptide, can be made without altering the function of the polypeptide, these conservative variants are, likewise, a feature of the invention.

For example, substitutions, deletions and insertions introduced into the sequences provided in the Sequence Listing are also envisioned by the invention. Such sequence modifications can be engineered into a sequence by site-directed mutagenesis (Wu (ed.) Meth. Enzymol. (1993) vol. 217, Academic Press) or the other methods noted below. Amino acid substitutions are typically of single residues; insertions usually will be on the order of about from 1 to 10 amino acid residues; and deletions will range about from 1 to 30 residues. In preferred embodiments, deletions or insertions are made in adjacent pairs, e.g., a deletion of two residues or insertion of two residues. Substitutions, deletions, insertions or any combination thereof can be combined to arrive at a sequence. The mutations that are made in the polynucleotide encoding the transcription factor should not place the sequence out of reading frame and should not create complementary regions that could produce secondary mRNA structure. Preferably, the polypeptide encoded by the DNA performs the desired function.

Conservative substitutions are those in which at least one residue in the amino acid sequence has been removed and a different residue inserted in its place. Such substitutions generally are made in accordance with the Table 4 when it is desired to maintain the activity of the protein. Table 4 shows amino acids which can be substituted for an amino acid in a protein and which are typically regarded as conservative substitutions.

Table 4

Residue	Conservative Substitutions
Ala	Ser
Arg	Lys
Asn	Gln; His
Asp	Glu
Gln	Asn
Cys	Ser
Glu	Asp
Gly	Pro
His	Asn; Gln
Ile	Leu, Val
Leu	Ile; Val
Lys	Arg; Gln
Met	Leu; Ile
Phe	Met; Leu; Tyr
Ser	Thr; Gly
Thr	Ser;Val
Trp	Tyr
Tyr	Trp; Phe
Val	Ile; Leu

Substitutions that are less conservative than those in Table 4 can be selected by picking residues that differ more significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. The substitutions which in general are expected to produce the greatest changes in protein properties will be those in which (a) a hydrophilic residue, e.g., seryl or threonyl, is substituted for (or by) a hydrophobic residue, e.g., leucyl, isoleucyl, phenylalanyl,

valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, e.g., lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g., glutamyl or aspartyl; or (d) a residue having a bulky side chain, e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine.

FURTHER MODIFYING SEQUENCES OF THE INVENTION—MUTATION/FORCED EVOLUTION

In addition to generating silent or conservative substitutions as noted, above, the present invention optionally includes methods of modifying the sequences of the Sequence Listing. In the methods, nucleic acid or protein modification methods are used to alter the given sequences to produce new sequences and/or to chemically or enzymatically modify given sequences to change the properties of the nucleic acids or proteins.

Thus, in one embodiment, given nucleic acid sequences are modified, e.g., according to standard mutagenesis or artificial evolution methods to produce modified sequences. For example, Ausubel, *supra*, provides additional details on mutagenesis methods. Artificial forced evolution methods are described, e.g., by Stemmer (1994) Nature 370:389-391, and Stemmer (1994) Proc. Natl. Acad. Sci. USA 91:10747-10751. Many other mutation and evolution methods are also available and expected to be within the skill of the practitioner.

Similarly, chemical or enzymatic alteration of expressed nucleic acids and polypeptides can be performed by standard methods. For example, sequence can be modified by addition of lipids, sugars, peptides, organic or inorganic compounds, by the inclusion of modified nucleotides or amino acids, or the like. For example, protein modification techniques are illustrated in Ausubel, *supra*. Further details on chemical and enzymatic modifications can be found herein. These modification methods can be used to modify any given sequence, or to modify any sequence produced by the various mutation and artificial evolution modification methods noted herein.

Accordingly, the invention provides for modification of any given nucleic acid by mutation, evolution, chemical or enzymatic modification, or other

available methods, as well as for the products produced by practicing such methods, e.g., using the sequences herein as a starting substrate for the various modification approaches.

For example, optimized coding sequence containing codons preferred by a particular prokaryotic or eukaryotic host can be used e.g., to increase the rate of translation or to produce recombinant RNA transcripts having desirable properties, such as a longer half-life, as compared with transcripts produced using a non-optimized sequence. Translation stop codons can also be modified to reflect host preference. For example, preferred stop codons for *S. cerevisiae* and mammals are TAA and TGA, respectively. The preferred stop codon for monocotyledonous plants is TGA, whereas insects and *E. coli* prefer to use TAA as the stop codon.

The polynucleotide sequences of the present invention can also be engineered in order to alter a coding sequence for a variety of reasons, including but not limited to, alterations which modify the sequence to facilitate cloning, processing and/or expression of the gene product. For example, alterations are optionally introduced using techniques which are well known in the art, e.g., site-directed mutagenesis, to insert new restriction sites, to alter glycosylation patterns, to change codon preference, to introduce splice sites, etc.

Furthermore, a fragment or domain derived from any of the polypeptides of the invention can be combined with domains derived from other transcription factors or synthetic domains to modify the biological activity of a transcription factor. For instance, a DNA binding domain derived from a transcription factor of the invention can be combined with the activation domain of another transcription factor or with a synthetic activation domain. A transcription activation domain assists in initiating transcription from a DNA binding site. Examples include the transcription activation region of VP16 or GAL4 (Moore et al. (1998) Proc. Natl. Acad. Sci. USA 95: 376-381; and Aoyama et al. (1995) Plant Cell 7:1773-1785), peptides derived from bacterial sequences (Ma and Ptashne (1987) Cell 51; 113-119) and synthetic peptides (Giniger and Ptashne, (1987) Nature 330:670-672).

EXPRESSION AND MODIFICATION OF POLYPEPTIDES

Typically, polynucleotide sequences of the invention are incorporated into recombinant DNA (or RNA) molecules that direct expression of polypeptides of the invention in appropriate host cells, transgenic plants, in vitro translation systems, or the like. Due to the inherent degeneracy of the genetic code, nucleic acid sequences which encode substantially the same or a functionally equivalent amino acid sequence can be substituted for any listed sequence to provide for cloning and expressing the relevant homologue.

Vectors, Promoters and Expression Systems

The present invention includes recombinant constructs comprising one or more of the nucleic acid sequences herein. The constructs typically comprise a vector, such as a plasmid, a cosmid, a phage, a virus (e.g., a plant virus), a bacterial artificial chromosome (BAC), a yeast artificial chromosome (YAC), or the like, into which a nucleic acid sequence of the invention has been inserted, in a forward or reverse orientation. In a preferred aspect of this embodiment, the construct further comprises regulatory sequences, including, for example, a promoter, operably linked to the sequence. Large numbers of suitable vectors and promoters are known to those of skill in the art, and are commercially available.

General texts that describe molecular biological techniques useful herein, including the use and production of vectors, promoters and many other relevant topics, include Berger, Sambrook and Ausubel, *supra*. Any of the identified sequences can be incorporated into a cassette or vector, e.g., for expression in plants. A number of expression vectors suitable for stable transformation of plant cells or for the establishment of transgenic plants have been described including those described in Weissbach and Weissbach, (1989) Methods for Plant Molecular Biology, Academic Press, and Gelvin et al., (1990) Plant Molecular Biology Manual, Kluwer Academic Publishers. Specific examples include those derived from a Ti plasmid of *Agrobacterium tumefaciens*, as well as those disclosed by Herrera-Estrella et al. (1983) Nature 303: 209, Bevan (1984) Nucl Acid Res. 12: 8711-8721, Klee (1985) Bio/Technology 3: 637-642, for dicotyledonous plants.

Alternatively, non-Ti vectors can be used to transfer the DNA into monocotyledonous plants and cells by using free DNA delivery techniques. Such methods can involve, for example, the use of liposomes, electroporation, microprojectile bombardment, silicon carbide whiskers, and viruses. By using these methods transgenic plants such as wheat, rice (Christou (1991) Bio/Technology 9: 957-962) and corn (Gordon-Kamm (1990) Plant Cell 2: 603-618) can be produced. An immature embryo can also be a good target tissue for monocots for direct DNA delivery techniques by using the particle gun (Weeks et al. (1993) Plant Physiol 102: 1077-1084; Vasil (1993) Bio/Technology 10: 667-674; Wan and Lemeaux (1994) Plant Physiol 104: 37-48, and for Agrobacterium-mediated DNA transfer (Ishida et al. (1996) Nature Biotech 14: 745-750).

Typically, plant transformation vectors include one or more cloned plant coding sequence (genomic or cDNA) under the transcriptional control of 5' and 3' regulatory sequences and a dominant selectable marker. Such plant transformation vectors typically also contain a promoter (e.g., a regulatory region controlling inducible or constitutive, environmentally-or developmentally-regulated, or cell- or tissue-specific expression), a transcription initiation start site, an RNA processing signal (such as intron splice sites), a transcription termination site, and/or a polyadenylation signal.

Examples of constitutive plant promoters which can be useful for expressing the TF sequence include: the cauliflower mosaic virus (CaMV) 35S promoter, which confers constitutive, high-level expression in most plant tissues (*see,* e.g., Odel et al. (1985) Nature 313:810); the nopaline synthase promoter (An et al. (1988) Plant Physiol 88:547); and the octopine synthase promoter (Fromm et al. (1989) Plant Cell 1: 977).

A variety of plant gene promoters that regulate gene expression in response to environmental, hormonal, chemical, developmental signals, and in a tissue-specific or preferential manner can be used for expression of a TF sequence in plants. Choice of a promoter is based largely on the phenotype of interest and is determined by such factors as tissue (e.g., seed, fruit, root, pollen, vascular tissue, flower, carpel, etc.), inducibility (e.g., in response to wounding, heat, cold, drought, light, pathogens, etc.), timing, developmental stage, and the like. Numerous known

promoters have been characterized and can favorable be employed to promote expression of a polynucleotide of the invention in a transgenic plant or cell of interest. For example, tissue specific promoters include: seed-specific promoters (such as the napin, phaseolin or DC3 promoter described in US Pat. No. 5,773,697), fruit-specific promoters that are active during fruit ripening (such as the dru 1 promoter (US Pat. No. 5,783,393), or the 2A11 promoter (US Pat. No. 4,943,674) and the tomato polygalacturonase promoter (Bird et al. (1988) Plant Mol Biol 11:651), root-specific promoters, such as those disclosed in US Patent Nos. 5,618,988, 5,837,848 and 5,905,186, pollen-active promoters such as PTA29, PTA26 and PTA13 (US Pat. No. 5,792,929), promoters active in vascular tissue (Ringli and Keller (1998) Plant Mol Biol 37:977-988), flower-specific (Kaiser et al, (1995) Plant Mol Biol 28:231-243), pollen (Baerson et al. (1994) Plant Mol Biol 26:1947-1959), carpels (Ohl et al. (1990) Plant Cell 2:837-848), pollen and ovules (Baerson et al. (1993) Plant Mol Biol 22:255-267), auxin-inducible promoters (such as that described in van der Kop et al. (1999) Plant Mol Biol 39:979-990 or Baumann et al. (1999) Plant Cell 11:323-334), cytokinin-inducible promoter (Guevara-Garcia (1998) Plant Mol Biol 38:743-753), promoters responsive to gibberellin (Shi et al. (1998) Plant Mol Biol 38:1053-1060, Willmott et al. (1998) 38:817-825) and the like. Additional promoters are those that elicit expression in response to heat (Ainley et al. (1993) Plant Mol Biol 22: 13-23), light (e.g., the pea rbcS-3A promoter, Kuhlemeier et al. (1989) Plant Cell 1:471, and the maize rbcS promoter, Schaffner and Sheen (1991) Plant Cell 3: 997); wounding (e.g., *wunI*, Siebertz et al. (1989) Plant Cell 1: 961); pathogens (such as the PR-1 promoter described in Buchel et al. (1999) Plant Mol. Biol. 40:387-396, and the PDF1.2 promoter described in Manners et al. (1998) Plant Mol. Biol. 38:1071-80), and chemicals such as methyl jasmonate or salicylic acid (Gatz et al. (1997) Ann. Rev. Plant Physiol. Plant Mol Biol 48: 89-108). In addition, the timing of the expression can be controlled by using promoters such as those acting at senescence (Gan and Amasino (1995) Science 270: 1986-1988); or late seed development (Odell et al. (1994) Plant Physiol 106:447-458).

Plant expression vectors can also include RNA processing signals that can be positioned within, upstream or downstream of the coding sequence. In addition, the expression vectors can include additional regulatory sequences from the

3'-untranslated region of plant genes, e.g., a 3' terminator region to increase mRNA stability of the mRNA, such as the PI-II terminator region of potato or the octopine or nopaline synthase 3' terminator regions.

Additional Expression Elements

Specific initiation signals can aid in efficient translation of coding sequences. These signals can include, e.g., the ATG initiation codon and adjacent sequences. In cases where a coding sequence, its initiation codon and upstream sequences are inserted into the appropriate expression vector, no additional translational control signals may be needed. However, in cases where only coding sequence (e.g., a mature protein coding sequence), or a portion thereof, is inserted, exogenous transcriptional control signals including the ATG initiation codon can be separately provided. The initiation codon is provided in the correct reading frame to facilitate transcription. Exogenous transcriptional elements and initiation codons can be of various origins, both natural and synthetic. The efficiency of expression can be enhanced by the inclusion of enhancers appropriate to the cell system in use.

Expression Hosts

The present invention also relates to host cells which are transduced with vectors of the invention, and the production of polypeptides of the invention (including fragments thereof) by recombinant techniques. Host cells are genetically engineered (i.e., nucleic acids are introduced, e.g., transduced, transformed or transfected) with the vectors of this invention, which may be, for example, a cloning vector or an expression vector comprising the relevant nucleic acids herein. The vector is optionally a plasmid, a viral particle, a phage, a naked nucleic acids, *etc.* The engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants, or amplifying the relevant gene. The culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression, and will be apparent to those skilled in the art and in the references cited herein, including, Sambrook and Ausubel.

The host cell can be a eukaryotic cell, such as a yeast cell, or a plant cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Plant

protoplasts are also suitable for some applications. For example, the DNA fragments are introduced into plant tissues, cultured plant cells or plant protoplasts by standard methods including electroporation (Fromm et al., (1985) Proc. Natl. Acad. Sci. USA 82, 5824, infection by viral vectors such as cauliflower mosaic virus (CaMV) (Hohn et al., (1982) Molecular Biology of Plant Tumors, (Academic Press, New York) pp. 549-560; US 4,407,956), high velocity ballistic penetration by small particles with the nucleic acid either within the matrix of small beads or particles, or on the surface (Klein et al., (1987) Nature 327, 70-73), use of pollen as vector (WO 85/01856), or use of *Agrobacterium tumefaciens* or *A. rhizogenes* carrying a T-DNA plasmid in which DNA fragments are cloned. The T-DNA plasmid is transmitted to plant cells upon infection by *Agrobacterium tumefaciens*, and a portion is stably integrated into the plant genome (Horsch et al. (1984) Science 233:496-498; Fraley et al. (1983) Proc. Natl. Acad. Sci. USA 80, 4803).

The cell can include a nucleic acid of the invention which encodes a polypeptide, wherein the cells expresses a polypeptide of the invention. The cell can also include vector sequences, or the like. Furthermore, cells and transgenic plants which include any polypeptide or nucleic acid above or throughout this specification, e.g., produced by transduction of a vector of the invention, are an additional feature of the invention.

For long-term, high-yield production of recombinant proteins, stable expression can be used. Host cells transformed with a nucleotide sequence encoding a polypeptide of the invention are optionally cultured under conditions suitable for the expression and recovery of the encoded protein from cell culture. The protein or fragment thereof produced by a recombinant cell may be secreted, membrane-bound, or contained intracellularly, depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides encoding mature proteins of the invention can be designed with signal sequences which direct secretion of the mature polypeptides through a prokaryotic or eukaryotic cell membrane.

IDENTIFICATION OF ADDITIONAL FACTORS

A transcription factor provided by the present invention can also be used to identify additional endogenous or exogenous molecules that can affect a phenotype or trait of interest. On the one hand, such molecules include organic (small or large molecules) and/or inorganic compounds that affect expression of (i.e., regulate) a particular transcription factor. Alternatively, such molecules include endogenous molecules that are acted upon either at a transcriptional level by a transcription factor of the invention to modify a phenotype as desired. For example, the transcription factors can be employed to identify one or more downstream gene with which is subject to a regulatory effect of the transcription factor. In one approach, a transcription factor or transcription factor homologue of the invention is expressed in a host cell, e.g., a transgenic plant cell, tissue or explant, and expression products, either RNA or protein, of likely or random targets are monitored, e.g., by hybridization to a microarray of nucleic acid probes corresponding to genes expressed in a tissue or cell type of interest, by two-dimensional gel electrophoresis of protein products, or by any other method known in the art for assessing expression of gene products at the level of RNA or protein. Alternatively, a transcription factor of the invention can be used to identify promoter sequences (i.e., binding sites) involved in the regulation of a downstream target. After identifying a promoter sequence, interactions between the transcription factor and the promoter sequence can be modified by changing specific nucleotides in the promoter sequence or specific amino acids in the transcription factor that interact with the promoter sequence to alter a plant trait. Typically, transcription factor DNA binding sites are identified by gel shift assays. After identifying the promoter regions, the promoter region sequences can be employed in double-stranded DNA arrays to identify molecules that affect the interactions of the transcription factors with their promoters (Bulyk et al. (1999) Nature Biotechnology 17:573-577).

The identified transcription factors are also useful to identify proteins that modify the activity of the transcription factor. Such modification can occur by covalent modification, such as by phosphorylation, or by protein-protein (homo or-heteropolymer) interactions. Any method suitable for detecting protein-protein

interactions can be employed. Among the methods that can be employed are coimmunoprecipitation, cross-linking and co-purification through gradients or chromatographic columns, and the two-hybrid yeast system.

The two-hybrid system detects protein interactions in vivo and is described in Chien, et al., (1991), Proc. Natl. Acad. Sci. USA 88, 9578-9582 and is commercially available from Clontech (Palo Alto, Calif.). In such a system, plasmids are constructed that encode two hybrid proteins: one consists of the DNA-binding domain of a transcription activator protein fused to the TF polypeptide and the other consists of the transcription activator protein's activation domain fused to an unknown protein that is encoded by a cDNA that has been recombined into the plasmid as part of a cDNA library. The DNA-binding domain fusion plasmid and the cDNA library are transformed into a strain of the yeast *Saccharomyces cerevisiae* that contains a reporter gene (e.g., lacZ) whose regulatory region contains the transcription activator's binding site. Either hybrid protein alone cannot activate transcription of the reporter gene. Interaction of the two hybrid proteins reconstitutes the functional activator protein and results in expression of the reporter gene, which is detected by an assay for the reporter gene product. Then, the library plasmids responsible for reporter gene expression are isolated and sequenced to identify the proteins encoded by the library plasmids. After identifying proteins that interact with the transcription factors, assays for compounds that interfere with the TF protein-protein interactions can be preformed.

IDENTIFICATION OF MODULATORS

In addition to the intracellular molecules described above, extracellular molecules that alter activity or expression of a transcription factor, either directly or indirectly, can be identified. For example, the methods can entail first placing a candidate molecule in contact with a plant or plant cell. The molecule can be introduced by topical administration, such as spraying or soaking of a plant, and then the molecule's effect on the expression or activity of the TF polypeptide or the expression of the polynucleotide monitored. Changes in the expression of the TF polypeptide can be monitored by use of polyclonal or monoclonal antibodies, gel electrophoresis or the like. Changes in the expression of the corresponding

polynucleotide sequence can be detected by use of microarrays, Northerns, quantitative PCR, or any other technique for monitoring changes in mRNA expression. These techniques are exemplified in Ausubel et al. (eds) Current Protocols in Molecular Biology, John Wiley & Sons (1998). Such changes in the expression levels can be correlated with modified plant traits and thus identified molecules can be useful for soaking or spraying on fruit, vegetable and grain crops to modify traits in plants.

Essentially any available composition can be tested for modulatory activity of expression or activity of any nucleic acid or polypeptide herein. Thus, available libraries of compounds such as chemicals, polypeptides, nucleic acids and the like can be tested for modulatory activity. Often, potential modulator compounds can be dissolved in aqueous or organic (e.g., DMSO-based) solutions for easy delivery to the cell or plant of interest in which the activity of the modulator is to be tested. Optionally, the assays are designed to screen large modulator composition libraries by automating the assay steps and providing compounds from any convenient source to assays, which are typically run in parallel (e.g., in microtiter formats on microtiter plates in robotic assays).

In one embodiment, high throughput screening methods involve providing a combinatorial library containing a large number of potential compounds (potential modulator compounds). Such "combinatorial chemical libraries" are then screened in one or more assays, as described herein, to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as target compounds.

A combinatorial chemical library can be, e.g., a collection of diverse chemical compounds generated by chemical synthesis or biological synthesis. For example, a combinatorial chemical library such as a polypeptide library is formed by combining a set of chemical building blocks (e.g., in one example, amino acids) in every possible way for a given compound length (i.e., the number of amino acids in a polypeptide compound of a set length). Exemplary libraries include peptide libraries, nucleic acid libraries, antibody libraries (see, e.g., Vaughn et al. (1996) Nature Biotechnology, 14(3):309-314 and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang et al. Science (1996) 274:1520-1522 and U.S. Patent 5,593,853), peptide

nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), and small organic molecule libraries (see, e.g., benzodiazepines, Baum C&EN Jan 18, page 33 (1993); isoprenoids, U.S. Patent 5,569,588; thiazolidinones and metathiazanones, U.S. Patent 5,549,974; pyrrolidines, U.S. Patents 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent 5,506,337) and the like.

Preparation and screening of combinatorial or other libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent 5,010,175, Furka, Int. J. Pept. Prot. Res. 37:487-493 (1991) and Houghton et al. Nature 354:84-88 (1991)). Other chemistries for generating chemical diversity libraries can also be used.

In addition, as noted, compound screening equipment for high-throughput screening is generally available, e.g., using any of a number of well known robotic systems that have also been developed for solution phase chemistries useful in assay systems. These systems include automated workstations including an automated synthesis apparatus and robotic systems utilizing robotic arms. Any of the above devices are suitable for use with the present invention, e.g., for high-throughput screening of potential modulators. The nature and implementation of modifications to these devices (if any) so that they can operate as discussed herein will be apparent to persons skilled in the relevant art.

Indeed, entire high throughput screening systems are commercially available. These systems typically automate entire procedures including all sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. Similarly, microfluidic implementations of screening are also commercially available.

The manufacturers of such systems provide detailed protocols the various high throughput. Thus, for example, Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like. The integrated systems herein, in addition to providing for sequence alignment and, optionally, synthesis of relevant nucleic

acids, can include such screening apparatus to identify modulators that have an effect on one or more polynucleotides or polypeptides according to the present invention.

In some assays it is desirable to have positive controls to ensure that the components of the assays are working properly. At least two types of positive controls are appropriate. That is, known transcriptional activators or inhibitors can be incubated with cells/plants/ etc. in one sample of the assay, and the resulting increase/decrease in transcription can be detected by measuring the resulting increase in RNA/ protein expression, etc., according to the methods herein. It will be appreciated that modulators can also be combined with transcriptional activators or inhibitors to find modulators which inhibit transcriptional activation or transcriptional repression. Either expression of the nucleic acids and proteins herein or any additional nucleic acids or proteins activated by the nucleic acids or proteins herein, or both, can be monitored.

In an embodiment, the invention provides a method for identifying compositions that modulate the activity or expression of a polynucleotide or polypeptide of the invention. For example, a test compound, whether a small or large molecule, is placed in contact with a cell, plant (or plant tissue or explant), or composition comprising the polynucleotide or polypeptide of interest and a resulting effect on the cell, plant, (or tissue or explant) or composition is evaluated by monitoring, either directly or indirectly, one or more of: expression level of the polynucleotide or polypeptide, activity (or modulation of the activity) of the polynucleotide or polypeptide. In some cases, an alteration in a plant phenotype can be detected following contact of a plant (or plant cell, or tissue or explant) with the putative modulator, e.g., by modulation of expression or activity of a polynucleotide or polypeptide of the invention.

SUBSEQUENCES

Also contemplated are uses of polynucleotides, also referred to herein as oligonucleotides, typically having at least 12 bases, preferably at least 15, more preferably at least 20, 30, or 50 bases, which hybridize under at least highly stringent (or ultra-high stringent or ultra-ultra- high stringent conditions) conditions to a

polynucleotide sequence described above. The polynucleotides may be used as probes, primers, sense and antisense agents, and the like, according to methods as noted *supra*.

Subsequences of the polynucleotides of the invention, including polynucleotide fragments and oligonucleotides are useful as nucleic acid probes and primers. An oligonucleotide suitable for use as a probe or primer is at least about 15 nucleotides in length, more often at least about 18 nucleotides, often at least about 21 nucleotides, frequently at least about 30 nucleotides, or about 40 nucleotides, or more in length. A nucleic acid probe is useful in hybridization protocols, e.g., to identify additional polypeptide homologues of the invention, including protocols for microarray experiments. Primers can be annealed to a complementary target DNA strand by nucleic acid hybridization to form a hybrid between the primer and the target DNA strand, and then extended along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification of a nucleic acid sequence, e.g., by the polymerase chain reaction (PCR) or other nucleic-acid amplification methods. See Sambrook and Ausubel, *supra*.

In addition, the invention includes an isolated or recombinant polypeptide including a subsequence of at least about 15 contiguous amino acids encoded by the recombinant or isolated polynucleotides of the invention. For example, such polypeptides, or domains or fragments thereof, can be used as immunogens, e.g., to produce antibodies specific for the polypeptide sequence, or as probes for detecting a sequence of interest. A subsequence can range in size from about 15 amino acids in length up to and including the full length of the polypeptide.

PRODUCTION OF TRANSGENIC PLANTS

Modification of Traits

The polynucleotides of the invention are favorably employed to produce transgenic plants with various traits, or characteristics, that have been modified in a desirable manner, e.g., to improve plant biomass. For example, alteration of expression levels or patterns (e.g., spatial or temporal expression patterns) of one or more of the transcription factors (or transcription factor homologues) of the invention, as compared with the levels of the same protein found

in a wild type plant, can be used to modify a plant's traits. An illustrative example of trait modification, improved plant biomass, by altering expression levels of a particular transcription factor is described further in the Examples and the Sequence Listing.

Antisense and Cosuppression Approaches

In addition to expression of the nucleic acids of the invention as gene replacement or plant phenotype modification nucleic acids, the nucleic acids are also useful for sense and anti-sense suppression of expression, e.g., to down-regulate expression of a nucleic acid of the invention, e.g., as a further mechanism for modulating plant phenotype. That is, the nucleic acids of the invention, or subsequences or anti-sense sequences thereof, can be used to block expression of naturally occurring homologous nucleic acids. A variety of sense and anti-sense technologies are known in the art, e.g., as set forth in Lichtenstein and Nellen (1997) Antisense Technology: A Practical Approach IRL Press at Oxford University, Oxford, England. In general, sense or anti-sense sequences are introduced into a cell, where they are optionally amplified, e.g., by transcription. Such sequences include both simple oligonucleotide sequences and catalytic sequences such as ribozymes.

For example, a reduction or elimination of expression (i.e., a "knock-out") of a transcription factor or transcription factor homologue polypeptide in a transgenic plant, e.g., to modify a plant trait, can be obtained by introducing an antisense construct corresponding to the polypeptide of interest as a cDNA. For antisense suppression, the transcription factor or homologue cDNA is arranged in reverse orientation (with respect to the coding sequence) relative to the promoter sequence in the expression vector. The introduced sequence need not be the full length cDNA or gene, and need not be identical to the cDNA or gene found in the plant type to be transformed. Typically, the antisense sequence need only be capable of hybridizing to the target gene or RNA of interest. Thus, where the introduced sequence is of shorter length, a higher degree of homology to the endogenous transcription factor sequence will be needed for effective antisense suppression. While antisense sequences of various lengths can be utilized, preferably, the introduced antisense sequence in the vector will be at least 30 nucleotides in length, and

improved antisense suppression will typically be observed as the length of the antisense sequence increases. Preferably, the length of the antisense sequence in the vector will be greater than 100 nucleotides. Transcription of an antisense construct as described results in the production of RNA molecules that are the reverse complement of mRNA molecules transcribed from the endogenous transcription factor gene in the plant cell.

Suppression of endogenous transcription factor gene expression can also be achieved using a ribozyme. Ribozymes are RNA molecules that possess highly specific endoribonuclease activity. The production and use of ribozymes are disclosed in U.S. Patent No. 4,987,071 and U.S. Patent No. 5,543,508. Synthetic ribozyme sequences including antisense RNAs can be used to confer RNA cleaving activity on the antisense RNA, such that endogenous mRNA molecules that hybridize to the antisense RNA are cleaved, which in turn leads to an enhanced antisense inhibition of endogenous gene expression.

Vectors in which RNA encoded by a transcription factor or transcription factor homologue cDNA is over-expressed can also be used to obtain co-suppression of a corresponding endogenous gene, e.g., in the manner described in U.S. Patent No. 5,231,020 to Jorgensen. Such co-suppression (also termed sense suppression) does not require that the entire transcription factor cDNA be introduced into the plant cells, nor does it require that the introduced sequence be exactly identical to the endogenous transcription factor gene of interest. However, as with antisense suppression, the suppressive efficiency will be enhanced as specificity of hybridization is increased, e.g., as the introduced sequence is lengthened, and/or as the sequence similarity between the introduced sequence and the endogenous transcription factor gene is increased.

Vectors expressing an untranslatable form of the transcription factor mRNA, e.g., sequences comprising one or more stop codon, or nonsense mutation) can also be used to suppress expression of an endogenous transcription factor, thereby reducing or eliminating it's activity and modifying one or more traits. Methods for producing such constructs are described in U.S. Patent No. 5,583,021. Preferably, such constructs are made by introducing a premature stop codon into the transcription

factor gene. Alternatively, a plant trait can be modified by gene silencing using double-strand RNA (Sharp (1999) Genes and Development 13: 139-141).

Another method for abolishing the expression of a gene is by insertion mutagenesis using the T-DNA of *Agrobacterium tumefaciens*. After generating the insertion mutants, the mutants can be screened to identify those containing the insertion in a transcription factor or transcription factor homologue gene. Plants containing a single transgene insertion event at the desired gene can be crossed to generate homozygous plants for the mutation (Koncz et al. (1992) Methods in Arabidopsis Research, World Scientific).

Alternatively, a plant phenotype can be altered by eliminating an endogenous gene, such as a transcription factor or transcription factor homologue, e.g., by homologous recombination (Kempin et al. (1997) Nature 389:802).

A plant trait can also be modified by using the cre-lox system (for example, as described in US Pat. No. 5,658,772). A plant genome can be modified to include first and second lox sites that are then contacted with a Cre recombinase. If the lox sites are in the same orientation, the intervening DNA sequence between the two sites is excised. If the lox sites are in the opposite orientation, the intervening sequence is inverted.

The polynucleotides and polypeptides of this invention can also be expressed in a plant in the absence of an expression cassette by manipulating the activity or expression level of the endogenous gene by other means. For example, by ectopically expressing a gene by T-DNA activation tagging (Ichikawa et al. (1997) Nature 390 698-701; Kakimoto et al. (1996) Science 274: 982-985). This method entails transforming a plant with a gene tag containing multiple transcriptional enhancers and once the tag has inserted into the genome, expression of a flanking gene coding sequence becomes deregulated. In another example, the transcriptional machinery in a plant can be modified so as to increase transcription levels of a polynucleotide of the invention (*See*, e.g., PCT Publications WO 96/06166 and WO 98/53057 which describe the modification of the DNA binding specificity of zinc finger proteins by changing particular amino acids in the DNA binding motif).

The transgenic plant can also include the cellular machinery or mechanisms necessary for expressing or altering the activity of a polypeptide encoded

by an endogenous gene, for example by altering the phosphorylation state of the polypeptide to maintain it in an activated state.

Transgenic plants (or plant cells, or plant explants, or plant tissues) incorporating the polynucleotides of the invention and/or expressing the polypeptides of the invention can be produced by a variety of well established techniques as described above. Following construction of a vector, most typically an expression cassette, including a polynucleotide, e.g., encoding a transcription factor or transcription factor homologue, of the invention, standard techniques can be used to introduce the polynucleotide into a plant, a plant cell, a plant explant or a plant tissue of interest. Optionally, the plant cell, explant or tissue can be regenerated to produce a transgenic plant.

The plant can be any higher plant, including gymnosperms, monocotyledonous and dicotyledenous plants. Suitable protocols are available for *Leguminosae* (alfalfa, soybean, clover, etc.), *Umbelliferae* (carrot, celery, parsnip), *Cruciferae* (cabbage, radish, rapeseed, broccoli, etc.), *Curcurbitaceae* (melons and cucumber), *Gramineae* (wheat, corn, rice, barley, millet, etc.), *Solanaceae* (potato, tomato, tobacco, peppers, etc.), and various other crops. See protocols described in Ammirato et al. (1984) Handbook of Plant Cell Culture –Crop Species. Macmillan Publ. Co. Shimamoto et al. (1989) Nature 338:274-276; Fromm et al. (1990) Bio/Technology 8:833-839; and Vasil et al. (1990) Bio/Technology 8:429-434.

Transformation and regeneration of both monocotyledonous and dicotyledonous plant cells is now routine, and the selection of the most appropriate transformation technique will be determined by the practitioner. The choice of method will vary with the type of plant to be transformed; those skilled in the art will recognize the suitability of particular methods for given plant types. Suitable methods can include, but are not limited to: electroporation of plant protoplasts; liposome-mediated transformation; polyethylene glycol (PEG) mediated transformation; transformation using viruses; micro-injection of plant cells; micro-projectile bombardment of plant cells; vacuum infiltration; and *Agrobacterium tumeficiens* mediated transformation. Transformation means introducing a nucleotide sequence in a plant in a manner to cause stable or transient expression of the sequence.

Successful examples of the modification of plant characteristics by transformation with cloned sequences which serve to illustrate the current knowledge in this field of technology, and which are herein incorporated by reference, include: U.S. Patent Nos. 5,571,706; 5,677,175; 5,510,471; 5,750,386; 5,597,945; 5,589,615; 5,750,871; 5,268,526; 5,780,708; 5,538,880; 5,773,269; 5,736,369 and 5,610,042.

Following transformation, plants are preferably selected using a dominant selectable marker incorporated into the transformation vector. Typically, such a marker will confer antibiotic or herbicide resistance on the transformed plants, and selection of transformants can be accomplished by exposing the plants to appropriate concentrations of the antibiotic or herbicide.

After transformed plants are selected and grown to maturity, those plants showing a modified trait are identified. The modified trait can be any of those traits described above. Additionally, to confirm that the modified trait is due to changes in expression levels or activity of the polypeptide or polynucleotide of the invention can be determined by analyzing mRNA expression using Northern blots, RT-PCR or microarrays, or protein expression using immunoblots or Western blots or gel shift assays.

INTEGRATED SYSTEMS—SEQUENCE IDENTITY

Additionally, the present invention may be an integrated system, computer or computer readable medium that comprises an instruction set for determining the identity of one or more sequences in a database. In addition, the instruction set can be used to generate or identify sequences that meet any specified criteria. Furthermore, the instruction set may be used to associate or link certain functional benefits, such as an improved plant biomass, with one or more identified sequence.

For example, the instruction set can include, e.g., a sequence comparison or other alignment program, e.g., an available program such as, for example, the Wisconsin Package Version 10.0, such as BLAST, FASTA, PILEUP, FINDPATTERNS or the like (GCG, Madison, WI). Public sequence databases such as GenBank, EMBL, Swiss-Prot and PIR or private sequence databases such as PhytoSeq (Incyte Pharmaceuticals, Palo Alto, CA) can be searched.

Alignment of sequences for comparison can be conducted by the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443, by the search for similarity method of Pearson and Lipman (1988) Proc. Natl. Acad. Sci. U.S.A. 85: 2444, by computerized implementations of these algorithms. After alignment, sequence comparisons between two (or more) polynucleotides or polypeptides are typically performed by comparing sequences of the two sequences over a comparison window to identify and compare local regions of sequence similarity. The comparison window can be a segment of at least about 20 contiguous positions, usually about 50 to about 200, more usually about 100 to about 150 contiguous positions. A description of the method is provided in Ausubel et al., *supra*.

A variety of methods of determining sequence relationships can be used, including manual alignment and computer assisted sequence alignment and analysis. This later approach is a preferred approach in the present invention, due to the increased throughput afforded by computer assisted methods. As noted above, a variety of computer programs for performing sequence alignment are available, or can be produced by one of skill.

One example algorithm that is suitable for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described in Altschul et al. J. Mol. Biol 215:403-410 (1990). Software for performing BLAST analyses is publicly available, e.g., through the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov/). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al., *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate

the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (*see* Henikoff & Henikoff (1989) Proc. Natl. Acad. Sci. USA 89:10915).

In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences (*see,* e.g., Karlin & Altschul (1993) Proc. Natl. Acad. Sci. USA 90:5873-5787). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence (and, therefore, in this context, homologous) if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.1, or less than about 0.01, and or even less than about 0.001. An additional example of a useful sequence alignment algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments. The program can align, e.g., up to 300 sequences of a maximum length of 5,000 letters.

The integrated system, or computer typically includes a user input interface allowing a user to selectively view one or more sequence records corresponding to the one or more character strings, as well as an instruction set which aligns the one or more character strings with each other or with an additional character string to identify one or more region of sequence similarity. The system may include a link of one or more character strings with a particular phenotype or gene function. Typically, the system includes a user readable output element which displays an alignment produced by the alignment instruction set.

The methods of this invention can be implemented in a localized or distributed computing environment. In a distributed environment, the methods may implemented on a single computer comprising multiple processors or on a multiplicity of computers. The computers can be linked, e.g. through a common bus, but more preferably the computer(s) are nodes on a network. The network can be a generalized or a dedicated local or wide-area network and, in certain preferred embodiments, the computers may be components of an intra-net or an internet.

Thus, the invention provides methods for identifying a sequence similar or homologous to one or more polynucleotides as noted herein, or one or more target polypeptides encoded by the polynucleotides, or otherwise noted herein and may include linking or associating a given plant phenotype or gene function with a sequence. In the methods, a sequence database is provided (locally or across an inter or intra net) and a query is made against the sequence database using the relevant sequences herein and associated plant phenotypes or gene functions.

Any sequence herein can be entered into the database, before or after querying the database. This provides for both expansion of the database and, if done before the querying step, for insertion of control sequences into the database. The control sequences can be detected by the query to ensure the general integrity of both the database and the query. As noted, the query can be performed using a web browser based interface. For example, the database can be a centralized public database such as those noted herein, and the querying can be done from a remote terminal or computer across an internet or intranet.

EXAMPLES

The following examples are intended to illustrate but not limit the present invention.

EXAMPLE I. FULL LENGTH GENE IDENTIFICATION AND CLONING

Putative transcription factor sequences (genomic or ESTs) related to known transcription factors were identified in the *Arabidopsis thaliana* GenBank database using the tblastn sequence analysis program using default parameters and a P-value cutoff threshold of –4 or –5 or lower, depending on the length of the query

sequence. Putative transcription factor sequence hits were then screened to identify those containing particular sequence strings. If the sequence hits contained such sequence strings, the sequences were confirmed as transcription factors.

Alternatively, Arabidopsis *thaliana* cDNA libraries derived from different tissues or treatments, or genomic libraries were screened to identify novel members of a transcription family using a low stringency hybridization approach. Probes were synthesized using gene specific primers in a standard PCR reaction (annealing temperature 60° C) and labeled with ^{32}P dCTP using the High Prime DNA Labeling Kit (Boehringer Mannheim). Purified radiolabelled probes were added to filters immersed in Church hybridization medium (0.5 M $NaPO_4$ pH 7.0, 7% SDS, 1 % w/v bovine serum albumin) and hybridized overnight at 60 °C with shaking. Filters were washed two times for 45 to 60 minutes with 1xSCC, 1% SDS at 60° C.

To identify additional sequence 5' or 3' of a partial cDNA sequence in a cDNA library, 5' and 3' rapid amplification of cDNA ends (RACE) was performed using the Marathon™ cDNA amplification kit (Clontech, Palo Alto, CA). Generally, the method entailed first isolating poly(A) mRNA, performing first and second strand cDNA synthesis to generate double stranded cDNA, blunting cDNA ends, followed by ligation of the Marathon™ Adaptor to the cDNA to form a library of adaptor-ligated ds cDNA.

Gene-specific primers were designed to be used along with adaptor specific primers for both 5' and 3' RACE reactions. Nested primers, rather than single primers, were used to increase PCR specificity. Using 5' and 3' RACE reactions, 5' and 3' RACE fragments were obtained, sequenced and cloned. The process can be repeated until 5' and 3' ends of the full-length gene were identified. Then the full-length cDNA was generated by PCR using primers specific to 5' and 3' ends of the gene by end-to-end PCR.

EXAMPLE II. CONSTRUCTION OF EXPRESSION VECTORS

The sequence was amplified from a genomic or cDNA library using primers specific to sequences upstream and downstream of the coding region. The expression vector was pMEN20 or pMEN65, which are both derived from pMON316 (Sanders et al, (1987) Nucleic Acids Research 15:1543-58) and contain the CaMV

35S promoter to express transgenes. To clone the sequence into the vector, both pMEN20 and the amplified DNA fragment were digested separately with SalI and NotI restriction enzymes at 37° C for 2 hours. The digestion products were subject to electrophoresis in a 0.8% agarose gel and visualized by ethidium bromide staining. The DNA fragments containing the sequence and the linearized plasmid were excised and purified by using a Qiaquick gel extraction kit (Qiagen, CA). The fragments of interest were ligated at a ratio of 3:1 (vector to insert). Ligation reactions using T4 DNA ligase (New England Biolabs, MA) were carried out at 16° C for 16 hours. The ligated DNAs were transformed into competent cells of the *E. coli* strain DH5alpha by using the heat shock method. The transformations were plated on LB plates containing 50 mg/l kanamycin (Sigma).

Individual colonies were grown overnight in five milliliters of LB broth containing 50 mg/l kanamycin at 37° C. Plasmid DNA was purified by using Qiaquick Mini Prep kits (Qiagen, CA).

EXAMPLE III. TRANSFORMATION OF *AGROBACTERIUM* WITH THE EXPRESSION VECTOR

After the plasmid vector containing the gene was constructed, the vector was used to transform *Agrobacterium tumefaciens* cells expressing the gene products. The stock of *Agrobacterium tumefaciens* cells for transformation was made as described by Nagel et al. (1990) FEMS Microbiol Letts. 67: 325-328. *Agrobacterium* strain ABI was grown in 250 ml LB medium (Sigma) overnight at 28°C with shaking until an absorbance (A_{600}) of 0.5 – 1.0 was reached. Cells were harvested by centrifugation at 4,000 x g for 15 min at 4° C. Cells were then resuspended in 250 μl chilled buffer (1 mM HEPES, pH adjusted to 7.0 with KOH). Cells were centrifuged again as described above and resuspended in 125 μl chilled buffer. Cells were then centrifuged and resuspended two more times in the same HEPES buffer as described above at a volume of 100 μl and 750 μl, respectively. Resuspended cells were then distributed into 40 μl aliquots, quickly frozen in liquid nitrogen, and stored at -80° C.

Agrobacterium cells were transformed with plasmids prepared as described above following the protocol described by Nagel et al. For each DNA

construct to be transformed, 50 – 100 ng DNA (generally resuspended in 10 mM Tris-HCl, 1 mM EDTA, pH 8.0) was mixed with 40 μl of *Agrobacterium* cells. The DNA/cell mixture was then transferred to a chilled cuvette with a 2mm electrode gap and subject to a 2.5 kV charge dissipated at 25 μF and 200 μF using a Gene Pulser II apparatus (Bio-Rad). After electroporation, cells were immediately resuspended in 1.0 ml LB and allowed to recover without antibiotic selection for 2 – 4 hours at 28° C in a shaking incubator. After recovery, cells were plated onto selective medium of LB broth containing 100 μg/ml spectinomycin (Sigma) and incubated for 24-48 hours at 28° C. Single colonies were then picked and inoculated in fresh medium. The presence of the plasmid construct was verified by PCR amplification and sequence analysis.

EXAMPLE IV. TRANSFORMATION OF *ARABIDOPSIS* PLANTS WITH A*GROBACTERIUM TUMEFACIENS* WITH EXPRESSION VECTOR

After transformation of *Agrobacterium tumefaciens* with plasmid vectors containing the gene, single *Agrobacterium* colonies were identified, propagated, and used to transform *Arabidopsis* plants. Briefly, 500 ml cultures of LB medium containing 50 mg/l kanamycin were inoculated with the colonies and grown at 28° C with shaking for 2 days until an absorbance (A_{600}) of > 2.0 is reached. Cells were then harvested by centrifugation at 4,000 x g for 10 min, and resuspended in infiltration medium (1/2 X Murashige and Skoog salts (Sigma), 1 X Gamborg's B-5 vitamins (Sigma), 5.0% (w/v) sucrose (Sigma), 0.044 μM benzylamino purine (Sigma), 200 μl/L Silwet L-77 (Lehle Seeds) until an absorbance (A_{600}) of 0.8 was reached.

Prior to transformation, *Arabidopsis thaliana* seeds (ecotype Columbia) were sown at a density of ~10 plants per 4" pot onto Pro-Mix BX potting medium (Hummert International) covered with fiberglass mesh (18 mm X 16 mm). Plants were grown under continuous illumination (50-75 μE/m²/sec) at 22-23° C with 65-70% relative humidity. After about 4 weeks, primary inflorescence stems (bolts) are cut off to encourage growth of multiple secondary bolts. After flowering of the mature secondary bolts, plants were prepared for transformation by removal of all siliques and opened flowers.

The pots were then immersed upside down in the mixture of *Agrobacterium* infiltration medium as described above for 30 sec, and placed on their sides to allow draining into a 1' x 2' flat surface covered with plastic wrap. After 24 h, the plastic wrap was removed and pots are turned upright. The immersion procedure was repeated one week later, for a total of two immersions per pot. Seeds were then collected from each transformation pot and analyzed following the protocol described below.

EXAMPLE V. IDENTIFICATION OF ARABIDOPSIS PRIMARY TRANSFORMANTS

Seeds collected from the transformation pots were sterilized essentially as follows. Seeds were dispersed into in a solution containing 0.1% (v/v) Triton X-100 (Sigma) and sterile H_2O and washed by shaking the suspension for 20 min. The wash solution was then drained and replaced with fresh wash solution to wash the seeds for 20 min with shaking. After removal of the second wash solution, a solution containing 0.1% (v/v) Triton X-100 and 70% ethanol (Equistar) was added to the seeds and the suspension was shaken for 5 min. After removal of the ethanol/detergent solution, a solution containing 0.1% (v/v) Triton X-100 and 30% (v/v) bleach (Clorox) was added to the seeds, and the suspension was shaken for 10 min. After removal of the bleach/detergent solution, seeds were then washed five times in sterile distilled H_2O. The seeds were stored in the last wash water at 4° C for 2 days in the dark before being plated onto antibiotic selection medium (1 X Murashige and Skoog salts (pH adjusted to 5.7 with 1M KOH), 1 X Gamborg's B-5 vitamins, 0.9% phytagar (Life Technologies), and 50 mg/l kanamycin). Seeds were germinated under continuous illumination (50-75 $\mu E/m^2/sec$) at 22-23° C. After 7-10 days of growth under these conditions, kanamycin resistant primary transformants (T_1 generation) were visible and obtained. These seedlings were transferred first to fresh selection plates where the seedlings continued to grow for 3-5 more days, and then to soil (Pro-Mix BX potting medium).

Primary transformants were crossed and progeny seeds (T_2) collected; kanamycin resistant seedlings were selected and analyzed. The expression levels of the recombinant polynucleotides in the transformants vary from about a 5%

expression level increase to a least a 100% expression level increase. Similar observations are made with respect to polypeptide level expression.

EXAMPLE VI. IDENTIFICATION OF ARABIDOPSIS PLANTS WITH TRANSCRIPTION FACTOR GENE KNOCKOUTS

The screening of insertion mutagenized *Arabidopsis* collections for null mutants in a known target gene was essentially as described in Krysan et al (1999) Plant Cell 11:2283-2290. Briefly, gene-specific primers, nested by 5-250 base pairs to each other, were designed from the 5' and 3' regions of a known target gene. Similarly, nested sets of primers were also created specific to each of the T-DNA or transposon ends (the "right" and "left" borders). All possible combinations of gene specific and T-DNA/transposon primers were used to detect by PCR an insertion event within or close to the target gene. The amplified DNA fragments were then sequenced which allows the precise determination of the T-DNA/transposon insertion point relative to the target gene. Insertion events within the coding or intervening sequence of the genes were deconvoluted from a pool comprising a plurality of insertion events to a single unique mutant plant for functional characterization. The method is described in more detail in Yu and Adam, US Application Serial No. 09/177,733 filed October 23, 1998.

EXAMPLE VII. IDENTIFICATION OF OVEREXPRESSOR OR GENE KNOCKOUT PLANTS WITH MODIFIED PLANT BIOMASS

Experiments were performed to identify those transformants or knockouts that exhibited a modified biomass phenotype. The plants were grown under continuous light conditions at 20-25° C. For such studies, the transformants' leaves and seeds were observed for a modified phenotype. For plant dry weight determination, a plant was place in an oven for 3 days at 65 to 70 °C.

We observed that plants overexpressing G1073 (SEQ ID NO: 1 and 2) constitutively (three independent T2 populations having 6 plants in one population and 16 plants in each of the other two) had increased biomass as measured by an increase in the plant fresh weight, the plant's dry weight or the seed yield compared with control plants transformed with an empty transformation vector under the control

of the 35S promoter. Typically, the plant fresh weight, dry weight or seed yield were increased by at least 150%.

We identified additional genes that are related to G1073 based on sequence identity and therefore are suitable for increasing plant biomass. The genes were G2789 (SEQ ID NO: 3 and 4), G1945 (SEQ ID NO: 5 and 6), and G2155 (SEQ ID NO: 7 and 8) . G2789 shares 89% sequence identity over a conserved domain of G1073 (amino acid residues 33 through 50 of SEQ ID NO: 2), whereas G1945 shares about an 89% sequence identity over the same domain and G2155 shares a 78% sequence identity over that domain. G2155 and G1945 share an 83% sequence identity over that region. To confirm that these related transcription factors could be used to modify plant biomass, we measured changes in plant biomass for G2155 or G2789 overexpressors. We observed that when either G2155 or G2789 were overexpressed in plants the transformed plants were substantially larger than the wild type plant.

Genes or sequences selected from Table 1 or Table 2 can also be overexpressed or knocked out in a plant to produce a plant with modified biomass. Preferably, the sequence selected (Test Sequence) from Table 1 or Table 2 is overexpressed in the same species listed for the selected sequences, however, another species may be used.

EXAMPLE VIII. IDENTIFICATION OF HOMOLOGOUS SEQUENCES

Homologous sequences from Arabidopsis and plant species other than Arabidopsis are identified using database sequence search tools, such as the Basic Local Alignment Search Tool (BLAST) (Altschul et al. (1990) J. Mol. Biol. 215:403-410; and Altschul et al. (1997) Nucl. Acid Res. 25: 3389-3402). The tblastx sequence analysis programs are employed using the BLOSUM-62 scoring matrix (Henikoff, S. and Henikoff, J. G. (1992) Proc. Natl. Acad. Sci. USA 89: 10915-10919).

Identified Arabidopsis homologous sequences are provided in Tables 1 and 2, appended to this application.. The percent sequence identity among these sequences can be as low as 47%, or even lower sequence identity. The entire NCBI GenBank database was filtered for sequences from all plants except *Arabidopsis thaliana* by selecting all entries in the NCBI GenBank database associated with NCBI

taxonomic ID 33090 (Viridiplantae; all plants) and excluding entries associated with taxonomic ID 3701 (*Arabidopsis thaliana*). These sequences were compared to sequences representing genes of SEQ ID NO: 1-8 using the Washington University TBLASTX algorithm (version 2.0a19MP) at the default settings using gapped alignments with the filter "off." For each gene of SEQ ID NO: 1-8, individual comparisons are ordered by probability score (P-value), where the score reflects the probability that a particular alignment occurred by chance. For example, a score of 3.6e-40 is 3.6 x 10-40. In addition to P-values, comparisons are also scored by percentage identity. Percentage identity reflects the degree to which two segments of DNA or protein are identical over a particular length.

Table 1 (appended to this application) lists a summary of orthologous and homologous sequences identified using BLAST (tblastx program) and the standard BLAST result data generated from a search. The first column shows the polynucleotide sequence identifier (SEQ ID NO), the second column shows the transcription factor cDNA identifier (Gene ID), the third column shows the GenBank Accession Number of the orthologous or homologous polynucleotide sequence identified in a BLAST search (Test Sequence ID), the fourth column shows the calculated probability value that the sequence identity is due to chance (Smallest Sum Probability), the fifth column identifies the plant species of the Test Sequence (Test Sequence Species), and the sixth column shows the GenBank annotation for the sequence identified in a BLAST search (Test Sequence GenBank Annotation).

Table 2 (appended to this application) lists orthologous and homologous sequences identified using BLAST (tblastx program) and the standard BLAST result data generated from a search. The first column shows the polynucleotide sequence identifier (SEQ ID NO), the second column shows the transcription factor cDNA identifier (Gene ID), the third column shows the GenBank Accession Number of the orthologous or homologous polynucleotide (Test Sequence ID), the fourth column shows the GenBank annotation for the sequence identified in a BLAST search (Test Sequence GenBank Annotation), the fifth column shows the reading frame of the Test sequence encoding the orthologous or homologous sequence (Reading Frame), the sixth column shows the calculated score value of the aligned sequences (High Score), the seventh column shows the calculated probability

value that the sequence identity is due to chance (Smallest Sum Probability), and the eighth column shows the number of regions in the Test Sequence that align with a sequence from the SEQ ID NO. (N).

All references, publications, patents and other documents and information sources herein are incorporated by reference in their entirety for all purposes. Although the invention has been described with reference to the embodiments and examples above, it should be understood that various modifications can be made without departing from the spirit of the invention.

Table 1 MBI-0034

SEQ ID NO	Gene ID	Test Sequence ID	Smallest Sum Probability	Test Sequence Species	Test Sequence GenBank Annotation
1	G1073	AP004165	4.10E-68	[Oryza sativa]	chromosome 2 clone OJ1479_B12, *** SEQUENCING
1	G1073	BH730050	1.10E-57	[Brassica oleracea]	BOMEB22TF BO_2_3_KB Brassica oleracea gen
1	G1073	BG134451	2.80E-57	[Lycopersicon esculentum]	EST467343 tomato crown gall Lycoper
1	G1073	BG581882	4.10E-57	[Medicago truncatula]	EST483618 GVN Medicago truncatula cDNA
1	G1073	BM110212	2.40E-54	[Solanum tuberosum]	EST557748 potato roots Solanum tuberosum
1	G1073	BI321563	7.00E-50	[Glycine max]	saf12g07.y3 Gm-c1076 Glycine max cDNA clone GEN
1	G1073	BF254863	3.70E-47	[Hordeum vulgare]	HVSMEf0005E05f Hordeum vulgare seedling roo
1	G1073	AW720668	5.50E-42	[Lotus japonicus]	LjNEST14h9rc Lotus japonicus nodule library
1	G1073	BF588135	6.10E-30	[Sorghum propinquum]	FM1_38_B09.b1_A003 Floral-Induced Merist
1	G1073	BH173434	4.10E-28	[Zea mays]	0104B13 maize genomic ORF library F Zea mays genom
1	G1073	gi15528814	2.60E-37	[Oryza sativa]	hypothetical protein~similar to Arabidopsis
1	G1073	gi2213536	5.50E-21	[Pisum sativum]	DNA-binding protein PD1.
1	G1073	gi4165183	2.70E-19	[Antirrhinum majus]	SAP1 protein.
1	G1073	gi1276971	1.80E-05	[Daucus carota]	glycine-rich protein.
1	G1073	gi19867	0.0002	[Nicotiana tabacum]	extensin (AA 1-620).
1	G1073	gi1155068	0.00031	[Brassica napus]	cell wall-plasma membrane linker protein.
1	G1073	gi168457	0.00078	[Zea mays]	cell wall protein (put.); putative.
1	G1073	gi6523547	0.0018	[Volvox carteri f. nagariensis]	hydroxyproline-rich glycopr
1	G1073	gi1166450	0.0028	[Lycopersicon esculentum]	Tfm5.
1	G1073	gi11545668	0.004	[Chlamydomonas reinhardtii]	CIA5.
3	G2789	AL366947	2.70E-58	[Medicago truncatula]	MtBA11B10F1 MtBA Medicago truncatula cD
3	G2789	AP003526	2.90E-58	[Oryza sativa]	chromosome 6 clone P0548D03, *** SEQUENCING IN
3	G2789	BM110212	6.10E-58	[Solanum tuberosum]	EST557748 potato roots Solanum tuberosum
3	G2789	BH664974	2.90E-57	[Brassica oleracea]	BOMBC11TF BO_2_3_KB Brassica oleracea gen
3	G2789	BG134451	9.70E-55	[Lycopersicon esculentum]	EST467343 tomato crown gall Lycoper
3	G2789	AW349284	2.00E-54	[Glycine max]	GM210004B21H7R Gm-r1021 Glycine max cDNA 3', mR
3	G2789	BF254863	3.70E-47	[Hordeum vulgare]	HVSMEf0005E05f Hordeum vulgare seedling roo
3	G2789	AW720668	2.40E-41	[Lotus japonicus]	LjNEST14h9rc Lotus japonicus nodule library
3	G2789	BJ203193	1.50E-29	[Physcomitrella patens subsp. patens]	BJ203193 normalized ful
3	G2789	BH173434	2.20E-27	[Zea mays]	0104B13 maize genomic ORF library F Zea mays genom

Table 1 MBI-0034

3	G2789	gi15528814	2.70E-35	[Oryza sativa]	hypothetical protein~similar to Arabidopsis
3	G2789	gi4165183	2.10E-19	[Antirrhinum majus]	SAP1 protein.
3	G2789	gi2213534	4.10E-18	[Pisum sativum]	DNA-binding PD1-like protein.
3	G2789	gi5679340	0.96	[Galega orientalis]	hypothetical protein.
5	G1945	BG647027	1.30E-59	[Medicago truncatula]	EST508646 HOGA Medicago truncatula cDNA
5	G1945	BH480897	1.80E-56	[Brassica oleracea]	BOGRA01TF BOGR Brassica oleracea genomic
5	G1945	BI426899	4.30E-48	[Glycine max]	sag08g12.y1 Gm-c1080 Glycine max cDNA clone GEN
5	G1945	OSJN00182	6.00E-44	[Oryza sativa]	chromosome 4 clone OSJNBa0086O06, *** SEQUENC
5	G1945	BI924382	1.70E-42	[Lycopersicon esculentum]	EST544271 tomato flower, buds 0-3 m
5	G1945	BM110212	1.50E-38	[Solanum tuberosum]	EST557748 potato roots Solanum tuberosum
5	G1945	BF254863	1.50E-34	[Hordeum vulgare]	HVSMEf0005E05f Hordeum vulgare seedling roo
5	G1945	AV411735	1.20E-33	[Lotus japonicus]	AV411735 Lotus japonicus young plants (two-
5	G1945	BJ203193	3.10E-27	[Physcomitrella patens subsp. patens]	BJ203193 normalized ful
5	G1945	BF588135	5.40E-22	[Sorghum propinquum]	FM1_38_B09.b1_A003 Floral-Induced Merist
5	G1945	gi15528814	1.10E-36	[Oryza sativa]	hypothetical protein~similar to Arabidopsis
5	G1945	gi4165183	4.60E-21	[Antirrhinum majus]	SAP1 protein.
5	G1945	gi2213534	8.70E-14	[Pisum sativum]	DNA-binding PD1-like protein.
5	G1945	gi100214	0.022	[Lycopersicon esculentum]	extensin class I (clone wY) - tom
5	G1945	gi13897322	0.12	[Zea mays]	somatic embryogenesis receptor-like kinase 3.
5	G1945	gi21992	0.14	[Volvox carteri]	extensin.
5	G1945	gi2108256	0.25	[Bromheadia finlaysoniana]	extensin.
5	G1945	gi6103625	0.28	[Picea rubens]	unknown.
5	G1945	gi310925	0.33	[Nicotiana tabacum]	cysteine-rich extensin-like protein-2.
5	G1945	gi168237	0.68	[Helianthus annuus]	hydroxyproline-rich protein.
7	G2155	BH480897	8.10E-61	[Brassica oleracea]	BOGRA01TF BOGR Brassica oleracea genomic
7	G2155	BG646893	8.80E-50	[Medicago truncatula]	EST508512 HOGA Medicago truncatula cDNA
7	G2155	BI426899	3.40E-39	[Glycine max]	sag08g12.y1 Gm-c1080 Glycine max cDNA clone GEN
7	G2155	AP004020	2.40E-38	[Oryza sativa]	chromosome 2 clone OJ1119_A01, *** SEQUENCING
7	G2155	BE432188	1.40E-34	[Lycopersicon esculentum]	EST398717 tomato breaker fruit, TIG
7	G2155	BM110212	2.70E-32	[Solanum tuberosum]	EST557748 potato roots Solanum tuberosum
7	G2155	AV411735	7.50E-30	[Lotus japonicus]	AV411735 Lotus japonicus young plants (two-
7	G2155	BF254863	1.00E-26	[Hordeum vulgare]	HVSMEf0005E05f Hordeum vulgare seedling roo
7	G2155	BJ203193	5.00E-20	[Physcomitrella patens subsp. patens]	BJ203193 normalized ful

Table 1 MBI-0034

7	G2155	BG465540	4.00E-19	[Sorghum propinquum]	RHIZ2_45_G09.b1_A003 Rhizome2 (RHIZ2) So
7	G2155	gi15528814	1.80E-31	[Oryza sativa]	hypothetical protein~similar to Arabidopsis
7	G2155	gi4165183	1.70E-19	[Antirrhinum majus]	SAP1 protein.
7	G2155	gi2213534	7.30E-16	[Pisum sativum]	DNA-binding PD1-like protein.
7	G2155	gi100214	0.12	[Lycopersicon esculentum]	extensin class I (clone wY) - tom
7	G2155	gi72327	0.2	[Zea mays]	glutelin 5 - maize.
7	G2155	gi3808062	0.47	[Cucurbita maxima]	PV100.
7	G2155	gi609288	0.74	[Zea diploperennis]	orf1.
7	G2155	gi2108256	0.84	[Bromheadia finlaysoniana]	extensin.
7	G2155	gi4666360	0.98	[Datisca glomerata]	zinc-finger protein 1.
7	G2155	gi17154773	0.99	[Cucumis sativus]	extensin-like protein.

Table 2 MBI-0034

SEQ ID NO	Gene ID	Test Sequence ID	Test Sequence GenBank Annotation	Reading Frame	High Score	Smallest Sum Probability	N
1	G1073	AP004165	AP004165 Oryza sativa chromosome 2 clone OJ1...	-3	721	4.10E-68	1
1	G1073	OSJN00182	AL662981 Oryza sativa chromosome 4 clone OSJ...	1	684	3.40E-64	1
1	G1073	AP004757	AP004757 Oryza sativa chromosome 6 clone P06...	-3	659	1.50E-61	1
1	G1073	BH730050	BH730050 BOMEB22TF BO_2_3_KB Brassica olerac...	-1	614	1.10E-57	1
1	G1073	BG134451	BG134451 EST467343 tomato crown gall Lycoper...	1	612	2.80E-57	1
1	G1073	BG581882	BG581882 EST483618 GVN Medicago truncatula c...	3	609	4.10E-57	1
1	G1073	AP004020	AP004020 Oryza sativa chromosome 2 clone OJ1...	2	616	5.40E-57	1
1	G1073	BH660108	BH660108 BOHVI48TF BO_2_3_KB Brassica olerac...	-1	595	1.10E-55	1
1	G1073	BH550632	BH550632 BOGUC18TR BOGU Brassica oleracea ge...	-2	594	1.40E-55	1
1	G1073	BH419879	BH419879 BOGGX69TF BOGG Brassica oleracea ge...	-2	588	6.60E-55	1
1	G1073	AW774484	AW774484 EST333635 KV3 Medicago truncatula c...	1	588	7.50E-55	1
1	G1073	AP004635	AP004635 Oryza sativa chromosome 8 clone P06...	-2	594	1.20E-54	1
1	G1073	AW574000	AW574000 EST316591 GVN Medicago truncatula c...	1	586	1.20E-54	1
1	G1073	BG583651	BG583651 EST485403 GVN Medicago truncatula c...	3	307	1.20E-54	3
1	G1073	BG647144	BG647144 EST508763 HOGA Medicago truncatula ...	1	585	1.40E-54	1
1	G1073	AP003526	AP003526 Oryza sativa chromosome 6 clone P05...	1	593	1.50E-54	1
1	G1073	AP004698	AP004698 Oryza sativa chromosome 8 clone P04...	2	591	2.40E-54	1
1	G1073	BM110212	BM110212 EST557748 potato roots Solanum tube...	1	583	2.40E-54	1
1	G1073	BH685875	BH685875 BOMBO90TR BO_2_3_KB Brassica olerac...	-1	578	9.60E-54	1
1	G1073	BH566718	BH566718 BOHCV23TR BOHC Brassica oleracea ge...	-2	575	1.70E-53	1
1	G1073	AL366947	AL366947 MtBA11B10F1 MtBA Medicago truncatul...	1	568	1.40E-52	1
1	G1073	AP003891	AP003891 Oryza sativa chromosome 8 clone OJ1...	2	573	2.00E-52	1
1	G1073	AP004587	AP004587 Oryza sativa chromosome 8 clone P05...	3	573	2.00E-52	1
1	G1073	BH729110	BH729110 BOHVN82TF BO_2_3_KB Brassica olerac...	-2	557	1.40E-51	1
1	G1073	BH459056	BH459056 BOGKX90TR BOGK Brassica oleracea ge...	-2	548	1.20E-50	1
1	G1073	BH717588	BH717588 BOMDB19TF BO_2_3_KB Brassica olerac...	2	547	1.80E-50	1
1	G1073	BI321563	BI321563 saf12g07.y3 Gm-c1076 Glycine max cD...	1	542	7.00E-50	1
1	G1073	BH481983	BH481983 BOGYI73TR BOGY Brassica oleracea ge...	2	536	2.20E-49	1
1	G1073	AW980581	AW980581 EST391734 GVN Medicago truncatula c...	3	526	3.10E-48	1
1	G1073	BE203784	BE203784 EST396460 KV0 Medicago truncatula c...	2	526	4.30E-48	1

Table 2 MBI-0034

1	G1073	AW776082	AW776082 EST335147 DSIL Medicago truncatula ...	3	522	8.80E-48	1
1	G1073	BF254863	BF254863 HVSMEf0005E05f Hordeum vulgare seed...	2	516	3.70E-47	1
1	G1073	BH664974	BH664974 BOMBC11TF BO_2_3_KB Brassica olerac...	2	514	4.50E-47	1
1	G1073	BG583687	BG583687 EST485440 GVN Medicago truncatula c...	2	513	6.10E-47	1
1	G1073	BH596283	BH596283 BOGBL42TR BOGB Brassica oleracea ge...	2	506	3.40E-46	1
1	G1073	BE999313	BE999313 EST431036 GVSN Medicago truncatula ...	1	395	7.20E-45	2
1	G1073	AW349284	AW349284 GM210004B21H7 Gm-r1021 Glycine max ...	-2	411	1.20E-44	2
1	G1073	BF067277	BF067277 st37f11.y1 Gm-c1067 Glycine max cDN...	3	489	4.10E-44	1
1	G1073	BF004270	BF004270 EST432768 KV1 Medicago truncatula c...	3	481	2.50E-43	1
1	G1073	BI701170	BI701170 sag55e11.y1 Gm-c1082 Glycine max cD...	2	478	4.00E-43	1
1	G1073	AP004680	AP004680 Oryza sativa chromosome 6 clone OSJ...	-1	266	5.50E-43	2
1	G1073	BH669958	BH669958 BOMEJ12TF BO_2_3_KB Brassica olerac...	1	478	5.70E-43	1
1	G1073	AW720668	AW720668 LjNEST14h9rc Lotus japonicus nodule...	1	467	5.50E-42	1
1	G1073	BH513264	BH513264 BOHQC93TR BOHQ Brassica oleracea ge...	-3	466	5.50E-42	1
1	G1073	AW350603	AW350603 GM210008B10B12 Gm-r1021 Glycine max...	-1	463	1.20E-41	1
1	G1073	BM779718	BM779718 EST590294 KV2 Medicago truncatula c...	-3	461	1.90E-41	1
1	G1073	BI419871	BI419871 LjNEST17a9r Lotus japonicus nodule ...	2	461	3.60E-41	1
1	G1073	BH550963	BH550963 BOHQE85TR BOHQ Brassica oleracea ge...	-3	458	3.80E-41	1
1	G1073	BG881387	BG881387 sae81e03.y1 Gm-c1065 Glycine max cD...	3	457	7.60E-41	1
1	G1073	BM526396	BM526396 sal40g01.y1 Gm-c1059 Glycine max cD...	3	456	9.50E-41	1
1	G1073	AW560824	AW560824 EST315872 DSIR Medicago truncatula ...	2	455	1.20E-40	1
1	G1073	BE998262	BE998262 EST429985 GVSN Medicago truncatula ...	2	426	1.40E-37	1
1	G1073	BM523502	BM523502 sam84f06.y2 Gm-c1087 Glycine max cD...	1	425	1.70E-37	1
1	G1073	BG646893	BG646893 EST508512 HOGA Medicago truncatula ...	2	422	2.80E-37	1
1	G1073	BH419964	BH419964 BOGQI28TF BOGQ Brassica oleracea ge...	-1	420	7.30E-37	1
1	G1073	AW774872	AW774872 EST334023 KV3 Medicago truncatula c...	3	413	4.60E-36	1
1	G1073	BH688757	BH688757 BOMDL66TF BO_2_3_KB Brassica olerac...	2	410	6.00E-36	1
1	G1073	AW780525	AW780525 sl72a07.y1 Gm-c1027 Glycine max cDN...	1	410	1.10E-35	1
1	G1073	AV422634	AV422634 AV422634 Lotus japonicus young plan...	3	406	2.20E-35	1
1	G1073	AP003938	AP003938 Oryza sativa chromosome 6 clone OJ1...	-2	405	1.30E-34	1
1	G1073	AP003683	AP003683 Oryza sativa genomic DNA, chromosom...	3	402	2.60E-34	1
1	G1073	BG647027	BG647027 EST508646 HOGA Medicago truncatula ...	3	393	2.90E-34	1
1	G1073	AW349908	AW349908 GM210006A20F9 Gm-r1021 Glycine max ...	-3	392	4.90E-34	1

Table 2 MBI-0034

1	G1073	AW621455	AW621455 EST312253 tomato root during/after ...	2	389	9.20E-34	1
1	G1073	BG599840	BG599840 EST504735 cSTS Solanum tuberosum cD...	3	205	2.20E-33	2
1	G1073	AP004319	AP004319 Oryza sativa chromosome 1 clone B10...	1	217	6.30E-32	2
1	G1073	AI736668	AI736668 sb32a03.y1 Gm-c1012 Glycine max cDN...	2	370	1.10E-31	1
1	G1073	AI494847	AI494847 sb06b09.y1 Gm-c1004 Glycine max cDN...	1	368	2.30E-31	1
1	G1073	BI426899	BI426899 sag08g12.y1 Gm-c1080 Glycine max cD...	1	367	2.40E-31	1
1	G1073	BF650426	BF650426 NF096G12EC1F1098 Elicited cell cult...	3	365	3.40E-31	1
1	G1073	BH430946	BH430946 BOHSM94TF BOHS Brassica oleracea ge...	-1	362	6.80E-31	1
1	G1073	BF588135	BF588135 FM1_38_B09.b1_A003 Floral-Induced M...	3	354	6.10E-30	1
1	G1073	AW348874	AW348874 GM210010A10G1 Gm-r1021 Glycine max ...	-2	352	7.20E-30	1
1	G1073	BM525692	BM525692 sak62d03.y1 Gm-c1036 Glycine max cD...	1	351	1.20E-29	1
1	G1073	BI970749	BI970749 GM830011A20H08 Gm-r1083 Glycine max...	-1	350	1.20E-29	1
1	G1073	BH679922	BH679922 BOMNO92TR BO_2_3_KB Brassica olerac...	3	348	1.80E-29	1
1	G1073	BG644865	BG644865 EST506484 KV3 Medicago truncatula c...	2	347	2.30E-29	1
1	G1073	BE020549	BE020549 sm45a11.y1 Gm-c1028 Glycine max cDN...	3	349	3.30E-29	1
1	G1073	AW648634	AW648634 EST327184 tomato germinating seedli...	3	343	8.50E-29	1
1	G1073	BH491363	BH491363 BOGPS71TR BOGP Brassica oleracea ge...	-1	338	2.10E-28	1
1	G1073	AV415346	AV415346 AV415346 Lotus japonicus young plan...	3	338	4.00E-28	1
1	G1073	BH173434	BH173434 0104B13 maize genomic ORF library F...	-1	339	4.10E-28	1
1	G1073	BI308126	BI308126 EST529536 GPOD Medicago truncatula ...	3	336	4.30E-28	1
1	G1073	BG600318	BG600318 EST505213 cSTS Solanum tuberosum cD...	1	333	1.80E-27	1
1	G1073	BE496294	BE496294 NXCI_022_C11_F NXCI (Nsf Xylem Comp...	1	330	2.40E-27	1
1	G1073	BI699513	BI699513 sag37g08.y1 Gm-c1081 Glycine max cD...	2	320	2.70E-26	1
1	G1073	BH480897	BH480897 BOGRA01TF BOGR Brassica oleracea ge...	-1	319	2.90E-26	1
1	G1073	AP004303	AP004303 Oryza sativa chromosome 7 clone P04...	2	323	6.20E-26	1
1	G1073	AI522924	AI522924 sa92b03.y1 Gm-c1004 Glycine max cDN...	2	312	2.10E-25	1
1	G1073	BH588550	BH588550 BOHOI48TR BOHO Brassica oleracea ge...	-2	310	2.30E-25	1
1	G1073	AW596625	AW596625 sj14f10.y1 Gm-c1032 Glycine max cDN...	2	310	2.80E-25	1
1	G1073	BI971972	BI971972 sag84f09.y1 Gm-c1084 Glycine max cD...	1	310	2.90E-25	1
1	G1073	BE432188	BE432188 EST398717 tomato breaker fruit, TIG...	3	309	3.70E-25	1
1	G1073	BE445433	BE445433 WHE1136_A09_B18ZS Wheat etiolated s...	2	304	1.20E-24	1
1	G1073	BI924382	BI924382 EST544271 tomato flower, buds 0-3 m...	3	304	1.40E-24	1
1	G1073	AP003917	AP003917 Oryza sativa chromosome 8 clone OJ1...	3	224	2.80E-24	2

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1	G1073	BE442709	BE442709 WHE1105_B09_C17ZS Wheat etiolated s...	3	299	4.00E-24	1
1	G1073	BG593477	BG593477 EST492155 cSTS Solanum tuberosum cD...	3	298	5.10E-24	1
1	G1073	BJ189956	BJ189956 BJ189956 normalized full length cDN...	3	297	5.80E-24	1
1	G1073	BH732637	BH732637 BOMBI03TF BO_2_3_KB Brassica olerac...	2	296	6.50E-24	1
1	G1073	BE342838	BE342838 EST395682 potato stolon, Cornell Un...	1	296	7.60E-24	1
1	G1073	BI786439	BI786439 sai49b05.y1 Gm-c1065 Glycine max cD...	1	295	1.10E-23	1
1	G1073	BM407572	BM407572 EST581899 potato roots Solanum tube...	1	219	1.70E-23	2
1	G1073	AW596434	AW596434 sj12d05.y1 Gm-c1032 Glycine max cDN...	2	293	2.50E-23	1
1	G1073	BE442615	BE442615 WHE1101_G09_M17ZS Wheat etiolated s...	2	289	4.70E-23	1
1	G1073	BG045781	BG045781 saa06a11.y1 Gm-c1058 Glycine max cD...	3	290	6.00E-23	1
1	G1073	AW776953	AW776953 EST336018 DSIL Medicago truncatula ...	2	279	4.90E-22	1
1	G1073	BM371214	BM371214 EBro04_SQ003_M20_R IGF Barley EBro0...	2	279	7.50E-22	1
1	G1073	BI972076	BI972076 sag85g11.y1 Gm-c1084 Glycine max cD...	2	277	8.50E-22	1
1	G1073	BI266587	BI266587 NF099D09IN1F1078 Insect herbivory M...	2	271	3.20E-21	1
1	G1073	BI406306	BI406306 159E11 Mature tuber lambda ZAP Sola...	1	270	4.50E-21	1
1	G1073	AV422959	AV422959 AV422959 Lotus japonicus young plan...	2	268	9.40E-21	1
1	G1073	BI699401	BI699401 sag36e12.y1 Gm-c1081 Glycine max cD...	-2	162	9.60E-21	2
1	G1073	BG465540	BG465540 RHIZ2_45_G09.b1_A003 Rhizome2 (RHIZ...	3	267	1.00E-20	1
1	G1073	AI522913	AI522913 sa91h08.y1 Gm-c1004 Glycine max cDN...	1	266	1.50E-20	1
1	G1073	AP003074	AP003074 Oryza sativa genomic DNA, chromosom...	-1	272	1.60E-20	1
1	G1073	AC007789	AC007789 Oryza sativa BAC OSJNBa0049B20 geno...	-1	272	1.60E-20	1
1	G1073	BI321153	BI321153 saf48b01.y3 Gm-c1077 Glycine max cD...	1	263	2.40E-20	1
1	G1073	BG596340	BG596340 EST495018 cSTS Solanum tuberosum cD...	3	262	2.80E-20	1
1	G1073	AW099294	AW099294 sd37h01.y1 Gm-c1016 Glycine max cDN...	2	264	4.10E-20	1
1	G1073	AV933535	AV933535 AV933535 K. Sato unpublished cDNA l...	1	257	9.80E-20	1
1	G1073	BF587149	BF587149 FM1_32_G07.b1_A003 Floral-Induced M...	3	258	1.10E-19	1
1	G1073	AW906401	AW906401 EST342523 potato stolon, Cornell Un...	2	256	1.60E-19	1
1	G1073	BI074657	BI074657 IP1_14_F04.b1_A002 Immature panicl...	1	255	1.70E-19	1
1	G1073	AW672482	AW672482 LG1_360_E08.b1_A002 Light Grown 1 (...	3	255	1.80E-19	1
1	G1073	AL373204	AL373204 MtBA56C11F1 MtBA Medicago truncatul...	3	253	3.60E-19	1
1	G1073	AV424890	AV424890 AV424890 Lotus japonicus young plan...	3	253	3.80E-19	1
1	G1073	BF324870	BF324870 su17c07.y1 Gm-c1066 Glycine max cDN...	1	252	4.50E-19	1
1	G1073	BM322182	BM322182 PIC1_1_A05.b1_A002 Pathogen-infecte...	2	250	5.60E-19	1

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1	G1073	BM322317	BM322317 PIC1_3_A06.b1_A002 Pathogen-infecte...	2	250	5.60E-19	1
1	G1073	BM322320	BM322320 PIC1_3_A09.b1_A002 Pathogen-infecte...	2	250	5.90E-19	1
1	G1073	BE496149	BE496149 WHE1262_H03_P06ZS Secale cereale an...	2	250	7.50E-19	1
1	G1073	BG583795	BG583795 EST485550 GVN Medicago truncatula c...	1	248	7.50E-19	1
1	G1073	BI974724	BI974724 sai72b06.y1 Gm-c1068 Glycine max cD...	1	245	2.00E-18	1
1	G1073	BM322319	BM322319 PIC1_3_A08.b1_A002 Pathogen-infecte...	2	245	2.10E-18	1
1	G1073	PSDBPPD1	X98738 P.sativum mRNA encoding DNA-binding p...	1	248	2.50E-18	1
1	G1073	BM322185	BM322185 PIC1_1_A08.b1_A002 Pathogen-infecte...	2	245	2.60E-18	1
1	G1073	BM322192	BM322192 PIC1_1_B08.b1_A002 Pathogen-infecte...	2	245	2.60E-18	1
1	G1073	BM322318	BM322318 PIC1_3_A07.b1_A002 Pathogen-infecte...	2	245	2.60E-18	1
1	G1073	AI965992	AI965992 sc25a12.y1 Gm-c1013 Glycine max cDN...	3	244	2.60E-18	1
1	G1073	BH596271	BH596271 BOGBL42TF BOGB Brassica oleracea ge...	-3	242	3.10E-18	1
1	G1073	AW309814	AW309814 sf25b03.x1 Gm-c1028 Glycine max cDN...	-1	242	3.50E-18	1
1	G1073	AL372048	AL372048 MtBA48C06F1 MtBA Medicago truncatul...	1	244	4.00E-18	1
1	G1073	BM079070	BM079070 MEST88-H11.T3 ISUM4-TN Zea mays cDN...	-1	241	4.20E-18	1
1	G1073	PSDBLPPD1	X98739 P.sativum mRNA encoding DNA-binding P...	1	244	4.40E-18	1
1	G1073	BG909764	BG909764 TaLr1108d02R TaLr1 Triticum aestivu...	3	242	4.70E-18	1
1	G1073	AW755604	AW755604 sl05h07.y1 Gm-c1036 Glycine max cDN...	3	241	5.30E-18	1
1	G1073	BF429428	BF429428 WHE1803_A09_B17ZS Secale cereale an...	1	242	5.60E-18	1
1	G1073	BE444180	BE444180 WHE1128_B06_D12ZS Wheat etiolated s...	2	241	6.20E-18	1
1	G1073	BG441060	BG441060 GA__Ea0011I19f Gossypium arboreum 7...	3	237	9.50E-18	1
1	G1073	BE587763	BE587763 WHE0652_C06_E12ZM Secale cereale ro...	1	239	1.00E-17	1
1	G1073	AW979681	AW979681 EST341290 tomato root deficiency, C...	1	236	1.80E-17	1
1	G1073	BE822274	BE822274 GM700017A10A4 Gm-r1070 Glycine max ...	-1	233	2.80E-17	1
1	G1073	BI139442	BI139442 F131P74Y Populus flower cDNA librar...	-1	233	4.10E-17	1
1	G1073	AMA132349	AJ132349 Antirrhinum majus mRNA for SAP1 pro...	3	232	4.60E-17	1
1	G1073	AW310124	AW310124 sf31d10.x1 Gm-c1028 Glycine max cDN...	-1	231	5.60E-17	1
1	G1073	BM322184	BM322184 PIC1_1_A07.b1_A002 Pathogen-infecte...	2	233	5.80E-17	1
1	G1073	AW622329	AW622329 EST313127 tomato root during/after ...	2	231	7.20E-17	1
1	G1073	BE600816	BE600816 PI1_90_E07.b1_A002 Pathogen induced...	3	229	1.00E-16	1
1	G1073	BG350206	BG350206 084D10 Mature tuber lambda ZAP Sola...	3	227	1.30E-16	1
1	G1073	BE357932	BE357932 DG1_23_D12.b1_A002 Dark Grown 1 (DG...	1	226	2.10E-16	1
1	G1073	AV917319	AV917319 AV917319 K. Sato unpublished cDNA l...	2	225	2.40E-16	1

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1	G1073	BF637181	BF637181 NF050F02LF1F1016 Developing leaf Me...	3	225	2.60E-16	1
1	G1073	AV411735	AV411735 AV411735 Lotus japonicus young plan...	1	226	2.80E-16	1
1	G1073	BE591277	BE591277 WHE1655-1658_J17_J17ZS Wheat heat s...	1	224	3.40E-16	1
1	G1073	BE125776	BE125776 DG1_57_B07.b1_A002 Dark Grown 1 (DG...	1	225	3.70E-16	1
1	G1073	BJ203193	BJ203193 BJ203193 normalized full length cDN...	1	224	3.80E-16	1
1	G1073	AW455702	AW455702 707090A08.x1 707 - Mixed adult tiss...	3	223	4.20E-16	1
1	G1073	BG241750	BG241750 RHIZ2_50_G05.b1_A003 Rhizome2 (RHIZ...	3	224	4.30E-16	1
1	G1073	BG589060	BG589060 EST490869 MHRP- Medicago truncatula...	1	222	4.40E-16	1
1	G1073	BI929403	BI929403 EST549292 tomato flower, 3 - 8 mm b...	1	220	6.30E-16	1
1	G1073	AW278127	AW278127 sf40a09.y1 Gm-c1009 Glycine max cDN...	1	222	6.60E-16	1
1	G1073	BI946361	BI946361 01104 leafy spurge Lambda HybriZAP ...	1	221	6.70E-16	1
1	G1073	BF625927	BF625927 HVSMEa0014H11f Hordeum vulgare seed...	1	221	8.40E-16	1
1	G1073	AI960613	AI960613 sc86h10.y1 Gm-c1018 Glycine max cDN...	1	221	8.60E-16	1
1	G1073	BE609898	BE609898 sq46e12.y1 Gm-c1019 Glycine max cDN...	3	219	1.20E-15	1
1	G1073	BE643892	BE643892 NXCI_048_F12_F NXCI (Nsf Xylem Comp...	3	218	2.00E-15	1
1	G1073	AL508367	AL508367 AL508367 Hordeum vulgare Barke deve...	3	214	3.50E-15	1
1	G1073	AW755831	AW755831 sl09h02.y1 Gm-c1036 Glycine max cDN...	3	214	5.50E-15	1
1	G1073	D42950	D42950 D42950 Rice callus cDNA (H.Uchimiya) ...	2	214	5.50E-15	1
1	G1073	BH677454	BH677454 BOHZJ50TR BO_2_3_KB Brassica olerac...	-3	210	7.10E-15	1
1	G1073	BM094106	BM094106 sah25e06.y1 Gm-c1036 Glycine max cD...	1	212	7.20E-15	1
1	G1073	BM358644	BM358644 GA__Ea0011I19r Gossypium arboreum 7...	3	211	7.40E-15	1
1	G1073	AW773741	AW773741 EST332727 KV3 Medicago truncatula c...	3	211	8.10E-15	1
1	G1073	BE807468	BE807468 ss22h03.y1 Gm-c1047 Glycine max cDN...	2	212	9.10E-15	1
1	G1073	BH650598	BH650598 BOHZR58TR BO_2_3_KB Brassica olerac...	1	210	9.60E-15	1
1	G1073	BM307331	BM307331 sak27h05.y1 Gm-c1075 Glycine max cD...	1	209	1.40E-14	1
1	G1073	BH510717	BH510717 BOGGW07TF BOGG Brassica oleracea ge...	1	208	1.50E-14	1
1	G1073	AW773742	AW773742 EST332728 KV3 Medicago truncatula c...	3	207	2.10E-14	1
1	G1073	BI267267	BI267267 NF100C06IN1F1070 Insect herbivory M...	2	137	2.20E-14	2
1	G1073	BE600623	BE600623 PI1_89_D08.b1_A002 Pathogen induced...	3	207	2.50E-14	1
1	G1073	AI881841	AI881841 606074A03.y1 606 - Ear tissue cDNA ...	3	206	2.60E-14	1
1	G1073	AW448258	AW448258 BRY_1522 BRY Triticum aestivum cDNA...	3	203	4.00E-14	1
1	G1073	BG132224	BG132224 EST465116 tomato crown gall Lycoper...	2	203	6.70E-14	1
1	G1073	BM086350	BM086350 sah38h08.y1 Gm-c1036 Glycine max cD...	3	202	7.40E-14	1

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1	G1073	AI443215	AI443215 sa45h07.y1 Gm-c1004 Glycine max cDN...	1	203	8.20E-14	1
1	G1073	BE345655	BE345655 946021H10.y2 946 - tassel primordiu...	3	201	9.60E-14	1
1	G1073	BH544467	BH544467 BOHKE60TF BOHK Brassica oleracea ge...	1	199	1.10E-13	1
1	G1073	BH572435	BH572435 BOHBY93TF BOHB Brassica oleracea ge...	1	199	1.20E-13	1
1	G1073	BI096714	BI096714 949019H11.y1 949 - Juvenile leaf an...	2	200	1.30E-13	1
1	G1073	BH439306	BH439306 BOHGL38TR BOHG Brassica oleracea ge...	1	199	1.60E-13	1
1	G1073	BE202989	BE202989 EST403011 KV1 Medicago truncatula c...	-3	199	1.60E-13	1
1	G1073	BE555817	BE555817 sp94c01.y1 Gm-c1045 Glycine max cDN...	3	199	1.70E-13	1
1	G1073	BG888793	BG888793 EST514644 cSTD Solanum tuberosum cD...	3	197	1.80E-13	1
1	G1073	BI788210	BI788210 sag68a10.y1 Gm-c1082 Glycine max cD...	3	196	3.10E-13	1
1	G1073	BE330349	BE330349 so77e09.y1 Gm-c1040 Glycine max cDN...	3	196	3.50E-13	1
1	G1073	BG352828	BG352828 sab91g04.y1 Gm-c1040 Glycine max cD...	3	196	3.60E-13	1
1	G1073	BG651836	BG651836 sad61f05.y1 Gm-c1051 Glycine max cD...	3	196	3.70E-13	1
1	G1073	BM094108	BM094108 sah25e08.y1 Gm-c1036 Glycine max cD...	1	195	4.70E-13	1
1	G1073	AW066510	AW066510 660015F03.y1 660 - Mixed stages of ...	1	194	6.00E-13	1
1	G1073	BG599554	BG599554 EST504449 cSTS Solanum tuberosum cD...	2	192	6.30E-13	1
1	G1073	AW928863	AW928863 EST337651 tomato flower buds 8 mm t...	3	193	6.90E-13	1
1	G1073	BM136003	BM136003 WHE2604_D04_H08ZS Wheat Fusarium gr...	-1	191	1.00E-12	1
1	G1073	BM521838	BM521838 sak76f11.y1 Gm-c1036 Glycine max cD...	2	191	1.10E-12	1
1	G1073	BE586257	BE586257 WHE501_B07_C13ZR Secale cereale alu...	2	190	1.30E-12	1
1	G1073	BF257835	BF257835 HVSMEf0014A01f Hordeum vulgare seed...	2	190	1.40E-12	1
1	G1073	BJ158045	BJ158045 BJ158045 full length cDNA library, ...	-3	190	1.40E-12	1
1	G1073	BG582457	BG582457 EST484202 GVN Medicago truncatula c...	3	190	2.10E-12	1
1	G1073	AI988292	AI988292 sc98f12.y1 Gm-c1020 Glycine max cDN...	2	188	2.20E-12	1
1	G1073	BG043009	BG043009 st91a08.y1 Gm-c1054 Glycine max cDN...	3	190	2.30E-12	1
1	G1073	AV410107	AV410107 AV410107 Lotus japonicus young plan...	2	189	2.80E-12	1
1	G1073	BG130143	BG130143 EST475789 tomato shoot/meristem Lyc...	1	186	3.00E-12	1
1	G1073	BF258208	BF258208 HVSMEf0015B16f Hordeum vulgare seed...	2	185	3.50E-12	1
1	G1073	BI435896	BI435896 EST538657 P. infestans-challenged l...	3	188	3.60E-12	1
1	G1073	BI700385	BI700385 sag60b11.y1 Gm-c1082 Glycine max cD...	2	187	3.70E-12	1
1	G1073	BF112609	BF112609 EST440199 tomato breaker fruit Lyco...	3	186	4.10E-12	1
1	G1073	BI469296	BI469296 sai10a11.y1 Gm-c1053 Glycine max cD...	3	186	4.50E-12	1
1	G1073	BJ186205	BJ186205 BJ186205 normalized full length cDN...	1	185	4.50E-12	1

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1	G1073	BE805340	BE805340 ss41d08.y1 Gm-c1061 Glycine max cDN...	1	186	5.30E-12	1
1	G1073	BG240061	BG240061 OV1_17_D10.b1_A002 Ovary 1 (OV1) So...	1	180	1.60E-11	1
1	G1073	BG240043	BG240043 OV1_17_B12.b1_A002 Ovary 1 (OV1) So...	1	180	1.70E-11	1
1	G1073	BM427899	BM427899 NXRV_006_A04_F NXRV (Nsf Xylem Root...	1	180	1.80E-11	1
1	G1073	BG240220	BG240220 OV1_19_D02.b1_A002 Ovary 1 (OV1) So...	1	180	2.10E-11	1
1	G1073	BG662369	BG662369 Ljirnpest43-456-c2 Ljirnp Lambda Hy...	1	184	2.10E-11	1
1	G1073	AW132605	AW132605 se06d10.y1 Gm-c1013 Glycine max cDN...	3	178	2.80E-11	1
1	G1073	BI932139	BI932139 EST552028 tomato flower, 8 mm to pr...	1	182	3.10E-11	1
1	G1073	HVU234403	AJ234403 Hordeum vulgare partial mRNA; clone...	1	175	5.10E-11	1
1	G1073	AW720136	AW720136 LjNEST14h9r Lotus japonicus nodule ...	1	175	7.60E-11	1
1	G1073	BG594217	BG594217 EST492895 cSTS Solanum tuberosum cD...	2	173	8.60E-11	1
1	G1073	BI972355	BI972355 sag90d06.y1 Gm-c1084 Glycine max cD...	2	173	9.90E-11	1
1	G1073	BM309583	BM309583 sak64c09.y1 Gm-c1036 Glycine max cD...	1	170	2.10E-10	1
1	G1073	BE639390	BE639390 946024E11.y1 946 - tassel primordiu...	1	169	2.60E-10	1
1	G1073	BM412174	BM412174 EST586501 tomato breaker fruit Lyco...	1	163	1.30E-09	1
1	G1073	BF636643	BF636643 NF091G07DT1F1055 Drought Medicago t...	1	164	1.30E-09	1
1	G1073	AW394835	AW394835 sh36a01.y1 Gm-c1017 Glycine max cDN...	2	162	2.10E-09	1
1	G1073	AI507693	AI507693 sb10d09.y1 Gm-c1004 Glycine max cDN...	2	161	2.70E-09	1
1	G1073	AW760534	AW760534 sl51e09.y1 Gm-c1027 Glycine max cDN...	1	157	7.30E-09	1
1	G1073	AV411140	AV411140 AV411140 Lotus japonicus young plan...	2	158	7.50E-09	1
1	G1073	AW223229	AW223229 EST300040 tomato fruit red ripe, TA...	1	156	9.10E-09	1
1	G1073	BG592977	BG592977 EST491655 cSTS Solanum tuberosum cD...	-2	155	1.20E-08	1
1	G1073	AI897688	AI897688 EST267131 tomato ovary, TAMU Lycope...	3	155	1.40E-08	1
1	G1073	BE923621	BE923621 EST427390 potato leaves and petiole...	1	155	1.50E-08	1
1	G1073	BM524672	BM524672 sal18d07.y1 Gm-c1059 Glycine max cD...	2	154	1.70E-08	1
1	G1073	BM524654	BM524654 sal18b12.y1 Gm-c1059 Glycine max cD...	2	154	1.80E-08	1
1	G1073	BF187248	BF187248 EST443535 potato stolon, Cornell Un...	2	154	1.90E-08	1
1	G1073	BE996884	BE996884 NXCI_103_F12_F NXCI (Nsf Xylem Comp...	1	155	2.20E-08	1
1	G1073	BE587194	BE587194 WHE0519_B07_D13ZR Secale cereale al...	1	155	2.30E-08	1
1	G1073	D15459	D15459 RICC0669A Rice callus Oryza sativa cD...	1	154	2.70E-08	1
1	G1073	AW776126	AW776126 EST335191 DSIL Medicago truncatula ...	2	163	3.00E-08	1
1	G1073	AW225998	AW225998 ST76B07 Pine TriplEx shoot tip libr...	2	152	3.30E-08	1
1	G1073	BE446692	BE446692 WHE1139_D09_H17ZS Wheat etiolated s...	2	152	3.70E-08	1

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1	G1073	BM341562	BM341562 MEST336-F03.T3 ISUM5-RN Zea mays cD...	-1	151	3.80E-08	1
1	G1073	AF474373	AF474373 Hordeum vulgare BAC 259I16, complet...	2	170	4.00E-08	1
1	G1073	BJ196157	BJ196157 BJ196157 normalized full length cDN...	1	153	4.20E-08	1
1	G1073	AV423934	AV423934 AV423934 Lotus japonicus young plan...	3	151	5.20E-08	1
1	G1073	BG604965	BG604965 WHE2325_E05_I09ZS Wheat pre-anthesi...	3	150	5.90E-08	1
1	G1073	AU198263	AU198263 AU198263 Rice green shoot Oryza sat...	1	150	5.90E-08	1
1	G1073	BG582452	BG582452 EST484197 GVN Medicago truncatula c...	3	161	6.40E-08	1
1	G1073	BM405827	BM405827 EST580154 potato roots Solanum tube...	2	150	6.50E-08	1
1	G1073	AI487942	AI487942 EST246264 tomato ovary, TAMU Lycope...	1	151	7.90E-08	1
1	G1073	BI931107	BI931107 EST550996 tomato flower, 8 mm to pr...	1	154	1.20E-07	1
1	G1073	BE923864	BE923864 EST427633 potato leaves and petiole...	1	147	1.40E-07	1
1	G1073	AW620872	AW620872 sj47g06.y1 Gm-c1033 Glycine max cDN...	3	147	1.40E-07	1
1	G1073	AW647786	AW647786 EST326240 tomato germinating seedli...	3	145	1.90E-07	1
1	G1073	BG098673	BG098673 EST463192 sprouting eyes/shoots Sol...	2	146	2.90E-07	1
1	G1073	AW761430	AW761430 sl67d09.y1 Gm-c1027 Glycine max cDN...	2	144	3.10E-07	1
1	G1073	AV421337	AV421337 AV421337 Lotus japonicus young plan...	2	145	3.60E-07	1
1	G1073	BF639276	BF639276 NF011F11IN1F1092 Insect herbivory M...	2	151	5.00E-07	1
1	G1073	AV425818	AV425818 AV425818 Lotus japonicus young plan...	3	142	5.40E-07	1
1	G1073	AI897113	AI897113 EST266556 tomato ovary, TAMU Lycope...	2	141	5.80E-07	1
1	G1073	BI928278	BI928278 EST548167 tomato flower, 3 - 8 mm b...	1	153	7.50E-07	1
1	G1073	BI929489	BI929489 EST549378 tomato flower, 3 - 8 mm b...	1	153	8.50E-07	1
1	G1073	BG601044	BG601044 EST505939 cSTS Solanum tuberosum cD...	1	141	9.80E-07	1
1	G1073	BG040551	BG040551 NXSI_112_D08_F NXSI (Nsf Xylem Side...	1	139	1.10E-06	1
1	G1073	BI927526	BI927526 EST547415 tomato flower, 3 - 8 mm b...	3	148	1.90E-06	1
1	G1073	BI788421	BI788421 sag70e10.y1 Gm-c1082 Glycine max cD...	3	135	3.00E-06	1
1	G1073	AW761107	AW761107 sl63c09.y1 Gm-c1027 Glycine max cDN...	1	135	3.90E-06	1
1	G1073	BG643949	BG643949 EST512143 tomato shoot/meristem Lyc...	2	146	5.10E-06	1
1	G1073	BG239709	BG239709 sab74e11.y1 Gm-c1032 Glycine max cD...	3	139	5.70E-06	1
1	G1073	BG149109	BG149109 48 LIN01 Lupinus luteus cDNA, mRNA ...	3	129	1.50E-05	1
1	G1073	BI308494	BI308494 EST529904 GPOD Medicago truncatula ...	2	143	1.60E-05	1
1	G1073	BG645337	BG645337 EST506956 KV3 Medicago truncatula c...	3	143	1.60E-05	1
1	G1073	AW031261	AW031261 EST274636 tomato callus, TAMU Lycop...	1	139	1.70E-05	1
1	G1073	AW164140	AW164140 Ljirnpest20-626-g4 Ljirnp Lambda Hy...	1	128	2.00E-05	1

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1	G1073	AL383224	AL383224 MtBC12G03F1 MtBC Medicago truncatul...	2	129	2.10E-05	1
1	G1073	BG275315	BG275315 NXSI_142_D09_F NXSI (Nsf Xylem Side...	3	129	2.30E-05	1
1	G1073	BH594393	BH594393 BOGKJ24TR BOGK Brassica oleracea ge...	-2	137	4.90E-05	1
1	G1073	D43486	D43486 D43486 Rice callus cDNA (H.Uchimiya) ...	3	125	7.80E-05	1
1	G1073	BM299690	BM299690 MCR053G12_23908 Ice plant Lambda Un...	2	134	9.80E-05	1
1	G1073	BG580062	BG580062 EST481784 GVN Medicago truncatula c...	2	129	0.00022	1
1	G1073	BI943944	BI943944 sa62b04.y1 Gm-c1004 Glycine max cDN...	2	118	0.00026	1
1	G1073	AC060755	AC060755 Oryza sativa chromosome 10 BAC OSJN...	-2	108	0.00028	2
1	G1073	AP004563	AP004563 Oryza sativa chromosome 8 clone P04...	-3	107	0.00037	2
1	G1073	BM112694	BM112694 EST560230 potato roots Solanum tube...	1	130	0.00046	1
1	G1073	AP004765	AP004765 Oryza sativa chromosome 8 clone P07...	-3	107	0.00049	2
1	G1073	BH467892	BH467892 BOGWZ38TF BOGW Brassica oleracea ge...	-3	115	0.00055	1
1	G1073	AI779587	AI779587 EST260466 tomato susceptible, Corne...	1	126	0.00064	1
1	G1073	BG856170	BG856170 1024044H01.y1 C. reinhardtii CC-169...	-2	128	0.00069	1
1	G1073	BG418060	BG418060 HVSMEk0021C01f Hordeum vulgare test...	3	129	0.00078	1
1	G1073	BE611882	BE611882 sr01b07.y1 Gm-c1049 Glycine max cDN...	1	111	0.0015	1
1	G1073	BM308752	BM308752 sak50a05.y1 Gm-c1036 Glycine max cD...	1	121	0.0018	1
1	G1073	AI691406	AI691406 606015E08.x1 606 - Ear tissue cDNA ...	-1	123	0.0021	1
1	G1073	AW698129	AW698129 NXNV_073_B01_F Nsf Xylem Normal woo...	1	111	0.0027	1
1	G1073	BH586480	BH586480 BOGPF83TR BOGP Brassica oleracea ge...	-1	123	0.004	1
1	G1073	BH423260	BH423260 BOGGZ42TF BOGG Brassica oleracea ge...	-2	120	0.0053	1
1	G1073	BH571929	BH571929 BOGTJ45TF BOGT Brassica oleracea ge...	-1	121	0.0062	1
1	G1073	AW216305	AW216305 687047G05.x1 687 - Early embryo fro...	-2	117	0.0083	1
1	G1073	AI939164	AI939164 sc67f03.y1 Gm-c1016 Glycine max cDN...	1	104	0.0099	1
1	G1073	BE454419	BE454419 HVSMEh0094G09f Hordeum vulgare 5-45...	1	119	0.013	1
1	G1073	BM112790	BM112790 EST560326 potato roots Solanum tube...	3	114	0.015	1
1	G1073	BG049445	BG049445 OV1_20_A09.g1_A002 Ovary 1 (OV1) So...	1	114	0.016	1
1	G1073	AP003925	AP003925 Oryza sativa chromosome 8 clone OJ1...	-2	121	0.017	1
1	G1073	AP004562	AP004562 Oryza sativa chromosome 8 clone P04...	-1	121	0.017	1
1	G1073	AW720219	AW720219 LjNEST17b3r Lotus japonicus nodule ...	1	113	0.021	1
1	G1073	BH218181	BH218181 1006077H06.x1 1006 - RescueMu Grid ...	1	106	0.026	1
1	G1073	BG647551	BG647551 EST509170 HOGA Medicago truncatula ...	2	112	0.027	1
1	G1073	BM078207	BM078207 MEST116-E03.T3 ISUM4-TN Zea mays cD...	-3	114	0.027	1

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1	G1073	AW929149	AW929149 EST337937 tomato flower buds 8 mm t...	2	114	0.03	1
1	G1073	BI310579	BI310579 EST5312329 GESD Medicago truncatula...	3	113	0.03	1
1	G1073	AW506972	AW506972 660056A02.x1 660 - Mixed stages of ...	-1	103	0.033	1
1	G1073	BI643921	BI643921 NXPV_129_D06_F NXPV (Nsf Xylem Plan...	1	101	0.038	1
1	G1073	AI441147	AI441147 sa59d03.y1 Gm-c1004 Glycine max cDN...	3	98	0.046	1
1	G1073	AQ577522	AQ577522 nbxb0091M13r CUGI Rice BAC Library ...	-1	111	0.054	1
1	G1073	BH723529	BH723529 BOMET92TR BO_2_3_KB Brassica olerac...	2	110	0.085	1
1	G1073	AL375620	AL375620 MtBB15H05F1 MtBB Medicago truncatul...	1	106	0.087	1
1	G1073	BF274574	BF274574 GA__Eb0021G20f Gossypium arboreum 7...	3	108	0.095	1
1	G1073	BF177556	BF177556 Ljirnpest31-487-f3 Ljirnp Lambda Hy...	3	95	0.12	1
1	G1073	AU067947	AU067947 AU067947 Rice callus Oryza sativa c...	-3	94	0.14	1
1	G1073	BM368289	BM368289 EBed01_SQ002_L11_R IGF Barley EBed0...	1	93	0.17	1
1	G1073	AP004116	AP004116 Oryza sativa chromosome 2 clone OJ1...	1	111	0.2	1
1	G1073	BI595695	BI595695 949022E11.x1 949 - Juvenile leaf an...	-2	91	0.26	1
1	G1073	BM417802	BM417802 952005G09.x11 952 - BMS tissue from...	1	91	0.28	1
1	G1073	BG649667	BG649667 RHIZ2_82_C04.b1_A003 Rhizome2 (RHIZ...	1	103	0.29	1
1	G1073	AC108762	AC108762 Oryza sativa chromosome 9 clone OSJ...	-3	109	0.3	1
1	G1073	BH698099	BH698099 BOMHI48TR BO_2_3_KB Brassica olerac...	-2	106	0.31	1
1	G1073	BI642324	BI642324 TZS924 TZS (Sapwood-heartwood trans...	-3	103	0.37	1
1	G1073	AW455681	AW455681 707089C04.x1 707 - Mixed adult tiss...	2	89	0.4	1
1	G1073	BE601230	BE601230 PI1_90_E07.g1_A002 Pathogen induced...	1	103	0.42	1
1	G1073	BE509974	BE509974 946069E12.y1 946 - tassel primordiu...	3	89	0.44	1
1	G1073	BH707416	BH707416 BOHTM48TR BO_2_3_KB Brassica olerac...	1	104	0.44	1
1	G1073	BM136703	BM136703 WHE0476_C06_E12ZS Wheat Fusarium gr...	3	88	0.46	1
1	G1073	BM093021	BM093021 saj04a05.y1 Gm-c1065 Glycine max cD...	3	100	0.48	1
1	G1073	BF274040	BF274040 GA__Eb0019P06f Gossypium arboreum 7...	3	103	0.49	1
1	G1073	BM404166	BM404166 EST578493 potato roots Solanum tube...	3	101	0.5	1
1	G1073	BH550347	BH550347 BOGPS25TR BOGP Brassica oleracea ge...	1	103	0.5	1
1	G1073	BF587998	BF587998 FM1_35_D12.g1_A003 Floral-Induced M...	2	101	0.51	1
1	G1073	AU097090	AU097090 AU097090 Rice shoot Oryza sativa cD...	2	100	0.54	1
1	G1073	BE643053	BE643053 Cri2_7_M09_SP6 Ceratopteris Spore L...	-3	103	0.56	1
1	G1073	BG051900	BG051900 RHIZ2_6_C11.g1_A003 Rhizome2 (RHIZ2...	1	101	0.56	1
1	G1073	BE455222	BE455222 HVSMEh0096K08f Hordeum vulgare 5-45...	-3	104	0.56	1

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1	G1073	BM377857	BM377857 EBem04_SQ004_G09_R IGF Barley EBem0...	2	97	0.56	1
1	G1073	AU181026	AU181026 AU181026 Rice green shoot Oryza sat...	3	87	0.63	1
1	G1073	AU197357	AU197357 AU197357 Rice panicle (between 3cm ...	-3	90	0.76	1
1	G1073	AI857154	AI857154 603007B08.x1 603 - stressed root cD...	1	99	0.76	1
1	G1073	AQ912903	AQ912903 nbeb0038P12r CUGI Rice BAC Library ...	2	92	0.77	1
1	G1073	BG859658	BG859658 1024064G02.y1 C. reinhardtii CC-169...	1	100	0.77	1
1	G1073	BI642507	BI642507 TZS128 TZS (Sapwood-heartwood trans...	1	100	0.8	1
1	G1073	BM377499	BM377499 EBem04_SQ003_F04_R IGF Barley EBem0...	2	95	0.81	1
1	G1073	AC091776	AC091776 Chlamydomonas reinhardtii clone cr-...	2	103	0.81	1
1	G1073	CNS07EFP	AL513405 Oryza sativa chromosome 12 clone OS...	3	103	0.81	1
1	G1073	AC087726	AC087726 Chlamydomonas reinhardtii clone cr-...	-2	103	0.81	1
1	G1073	BF256498	BF256498 HVSMEf0010C11f Hordeum vulgare seed...	-2	101	0.85	1
1	G1073	AI441317	AI441317 sa55c06.y1 Gm-c1004 Glycine max cDN...	3	84	0.86	1
1	G1073	BM377468	BM377468 EBem04_SQ003_D16_R IGF Barley EBem0...	3	93	0.86	1
1	G1073	AZ132443	AZ132443 OSJNBb0065J03r CUGI Rice BAC Librar...	1	99	0.87	1
1	G1073	AU181516	AU181516 AU181516 Rice callus (2001) Oryza s...	-2	94	0.89	1
1	G1073	BI722855	BI722855 1031064E12.x1 C. reinhardtii CC-169...	3	84	0.9	1
1	G1073	BF256757	BF256757 HVSMEf0010O19f Hordeum vulgare seed...	-1	100	0.9	1
1	G1073	BI779670	BI779670 EBem05_SQ001_A06_R IGF Barley EBem0...	2	83	0.91	1
1	G1073	BF256541	BF256541 HVSMEf0010E13f Hordeum vulgare seed...	-2	100	0.92	1
1	G1073	AU166731	AU166731 AU166731 Rice callus (2001) Oryza s...	-1	93	0.92	1
1	G1073	AU197773	AU197773 AU197773 Rice mature leaf Oryza sat...	2	83	0.93	1
1	G1073	BI478832	BI478832 952002B08.x10 952 - BMS tissue from...	2	91	0.94	1
1	G1073	C19731	C19731 C19731 Rice panicle at ripening stage...	3	83	0.95	1
1	G1073	AU181350	AU181350 AU181350 Rice callus (2001) Oryza s...	-1	93	0.95	1
1	G1073	BI779665	BI779665 EBem05_SQ001_A01_R IGF Barley EBem0...	3	83	0.96	1
1	G1073	BE421615	BE421615 HWM011cH.01r ITEC HWM Barley Leaf L...	-3	99	0.96	1
1	G1073	BM779307	BM779307 EST589882 KV2 Medicago truncatula c...	-1	94	0.97	1
1	G1073	AZ046505	AZ046505 nbeb0092I05f CUGI Rice BAC Library ...	-3	91	0.97	1
1	G1073	BI359024	BI359024 949054G08.x2 949 - Juvenile leaf an...	-3	94	0.97	1
1	G1073	BE577148	BE577148 L0-1863T3 Ice plant Lambda Uni-Zap ...	-2	94	0.98	1
1	G1073	BG343934	BG343934 HVSMEg0007C15f Hordeum vulgare pre-...	2	97	0.98	1
1	G1073	BI974612	BI974612 sai70g08.y1 Gm-c1068 Glycine max cD...	3	95	0.98	1

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1	G1073	BI948976	BI948976 HVSMEI0011O10f Hordeum vulgare spik...	1	98	0.98	1
1	G1073	BM417696	BM417696 952005B04.x10 952 - BMS tissue from...	1	91	0.98	1
1	G1073	BH740357	BH740357 qj75a08.b1 TO1000 Brassica oleracea...	-3	89	0.98	1
1	G1073	BE025350	BE025350 945025C05.Y1 945 - Mixed adult tiss...	-1	94	0.99	1
1	G1073	AQ689540	AQ689540 nbxb0079H20f CUGI Rice BAC Library ...	3	93	0.99	1
1	G1073	BE405965	BE405965 WHE0402_c07_c07zB Wheat etiolated s...	2	90	0.991	1
1	G1073	BE512087	BE512087 946066G03.x1 946 - tassel primordiu...	-1	88	0.991	1
1	G1073	BH716346	BH716346 BOMLG50TR BO_2_3_KB Brassica olerac...	3	82	0.993	1
1	G1073	BG442856	BG442856 GA__Ea0018I24f Gossypium arboreum 7...	-2	95	0.995	1
1	G1073	AI855566	AI855566 sc20h05.y1 Gm-c1013 Glycine max cDN...	2	91	0.995	1
1	G1073	BF256624	BF256624 HVSMEf0010I13f Hordeum vulgare seed...	-2	97	0.995	1
1	G1073	BG361509	BG361509 gb60d11.y1 Moss EST library PPG Phy...	-1	87	0.996	1
1	G1073	BM417834	BM417834 952005B04.x9 952 - BMS tissue from ...	2	87	0.996	1
1	G1073	BH739760	BH739760 gf19c08.b2 TO1000 Brassica oleracea...	-3	82	0.997	1
1	G1073	AQ867623	AQ867623 nbeb0032F15f CUGI Rice BAC Library ...	1	94	0.998	1
1	G1073	BF257444	BF257444 HVSMEf0012O23f Hordeum vulgare seed...	-1	96	0.9992	1
1	G1073	DCU47097	U47097 Daucus carota glycine-rich protein mR...	2	88	0.9994	1
1	G1073	AV933536	AV933536 AV933536 K. Sato unpublished cDNA I...	2	82	0.9994	1
1	G1073	BM737310	BM737310 952055A09.x1 952 - BMS tissue from ...	2	91	0.9996	1
1	G1073	BG309092	BG309092 HVSMEc0002B12f Hordeum vulgare seed...	1	94	0.9997	1
1	G1073	BE036544	BE036544 MP01B10 MP Mesembryanthemum crystal...	-1	95	0.9997	1
1	G1073	BE455291	BE455291 HVSMEh0096O24f Hordeum vulgare 5-45...	-2	95	0.9997	1
1	G1073	BF256580	BF256580 HVSMEf0010G11f Hordeum vulgare seed...	3	95	0.9997	1
1	G1073	C19642	C19642 C19642 Rice panicle at ripening stage...	1	90	0.9997	1
1	G1073	AI460865	AI460865 sa70c03.y1 Gm-c1004 Glycine max cDN...	3	90	0.9997	1
1	G1073	AQ257581	AQ257581 nbxb0018B13r CUGI Rice BAC Library ...	-1	94	0.9998	1
1	G1073	BE455156	BE455156 HVSMEh0096G12f Hordeum vulgare 5-45...	-1	95	0.9998	1
1	G1073	AW457868	AW457868 sh88c12.y1 Gm-c1016 Glycine max cDN...	1	87	0.9999	1
1	G1073	BE455227	BE455227 HVSMEh0096K18f Hordeum vulgare 5-45...	-2	95	0.9999	1
1	G1073	BI952821	BI952821 HVSMEm0007N22f Hordeum vulgare gree...	1	94	0.9999	1
1	G1073	BI957854	BI957854 HVSMEn0011M04f Hordeum vulgare rach...	-2	94	0.9999	1
1	G1073	AP004359	AP004359 Oryza sativa chromosome 1 clone B11...	-3	96	0.99994	1
1	G1073	AP003431	AP003431 Oryza sativa chromosome 1 clone B10...	1	96	0.99994	1

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1	G1073	AP004813	AP004813 Oryza sativa (japonica cultivar-gro...	1	96	0.99995	1
1	G1073	GI-15528814	hypothetical protein~similar to Arabidopsi...	-1	402	2.60E-37	1
1	G1073	GI-12643044	AC060755_3 putative AT-Hook DNA-binding pr...	-1	278	1.20E-27	2
1	G1073	GI-5042445	AC007789_8 hypothetical protein	-1	271	4.80E-24	2
1	G1073	GI-2213536	DNA-binding protein PD1	-1	248	5.50E-21	1
1	G1073	GI-7488825	T06584 probable DNA-binding protein - gard...	-1	248	5.50E-21	1
1	G1073	GI-2213534	DNA-binding PD1-like protein	-1	244	1.50E-20	1
1	G1073	GI-7488826	T06582 probable DNA-binding protein - gard...	-1	244	1.50E-20	1
1	G1073	GI-4165183	SAP1 protein	-1	232	2.70E-19	1
1	G1073	GI-1276971	glycine-rich protein	-3	107	1.80E-05	1
1	G1073	GI-7488920	T14306 glycine-rich protein - carrot (frag...	-3	107	1.80E-05	1
1	G1073	GI-19867	extensin (AA 1-620)	2	82	0.0002	3
1	G1073	GI-82169	S06733 hydroxyproline-rich glycoprotein pr...	2	82	0.0002	3
1	G1073	GI-119714	EXTN_TOBAC EXTENSIN PRECURSOR (CELL WALL H...	2	82	0.0002	3
1	G1073	GI-1155068	cell wall-plasma membrane linker protein	2	93	0.00031	3
1	G1073	GI-7446482	S71558 probable cell wall-plasma membrane ...	2	93	0.00031	3
1	G1073	GI-168457	cell wall protein (put.); putative	2	70	0.00078	3
1	G1073	GI-16924043	AC079179_10 Unknown protein [Oryza sativa]	2	94	0.0011	3
1	G1073	GI-6523547	hydroxyproline-rich glycoprotein DZ-HRGP	2	85	0.0018	3
1	G1073	GI-1166450	Tfm5	-1	82	0.0028	2
1	G1073	GI-7489011	T07381 glycine-rich protein Tfm5 - tomato	-1	82	0.0028	2
1	G1073	GI-20245	Glycine-rich protein	-1	82	0.0036	3
1	G1073	GI-72322	KNRZG2 glycine-rich cell wall structural p...	-1	82	0.0036	3
1	G1073	GI-232183	GRP2_ORYSA GLYCINE-RICH CELL WALL STRUCTUR...	-1	82	0.0036	3
1	G1073	GI-1167557	glycine-rich protein	-1	82	0.0036	3
1	G1073	GI-5917666	AF159297_1 extensin-like protein	2	104	0.0039	3
1	G1073	GI-11545668	AF317732_1 CIA5 [Chlamydomonas reinhardtii]	-1	78	0.004	3
1	G1073	GI-11875321	CCM1-B [Chlamydomonas reinhardtii]	-1	78	0.004	3
1	G1073	GI-11875325	CCM1-B [Chlamydomonas reinhardtii]	-1	78	0.004	3
1	G1073	GI-11875320	CCM1-A [Chlamydomonas reinhardtii]	-1	78	0.004	3
1	G1073	GI-11875323	CCM1-A [Chlamydomonas reinhardtii]	-1	78	0.004	3
1	G1073	GI-7008009	PsAD1	-1	85	0.0048	1
1	G1073	GI-22333	hydroxyproline-rich glycoprotein	2	70	0.0049	3

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1	G1073	GI-228936	1814452A Hyp-rich glycoprotein [Zea mays]	2	70	0.0049	3
1	G1073	GI-283045	S28264 hydroxyproline-rich glycoprotein - ...	2	70	0.0049	3
1	G1073	GI-22269	cell wall protein (108 AA)	2	68	0.0053	2
1	G1073	GI-100864	S08315 cell wall protein - maize (fragment)	2	68	0.0053	2
1	G1073	GI-168459	cell wall protein (put.); putative	2	68	0.0053	2
1	G1073	GI-227614	1707318A Thr rich extensin [Zea mays]	2	70	0.0068	3
1	G1073	GI-13277222	ZF-HD homeobox protein [Flaveria bidentis]	-1	87	0.0069	2
1	G1073	GI-228938	1814452C Hyp-rich glycoprotein [Zea diplop...	2	70	0.0084	3
1	G1073	GI-22508	cell wall protein (AA 1-267)	2	70	0.0088	3
1	G1073	GI-100863	S08314 cell wall glycoprotein - maize	2	70	0.0088	3
1	G1073	GI-119712	EXTN_MAIZE EXTENSIN PRECURSOR (PROLINE-RIC...	2	70	0.0088	3
1	G1073	GI-168455	cell wall protein (put.); putative	2	70	0.0088	3
1	G1073	GI-226756	1604465A cell wall protein [Zea mays]	2	70	0.0088	3
1	G1073	GI-228937	1814452B Hyp-rich glycoprotein [Zea mays]	2	70	0.01	3
1	G1073	GI-14549150	glycine-rich protein LeGRP1 [Lycopersicon ...	-1	85	0.012	3
1	G1073	GI-19929	pistil extensin like protein	2	78	0.012	2
1	G1073	GI-322761	JQ1696 pistil extensin-like protein precur...	2	78	0.012	2
1	G1073	GI-544262	EXLP_TOBAC PISTIL-SPECIFIC EXTENSIN-LIKE P...	2	78	0.012	2
1	G1073	GI-12083536	AC084218_15 hypothetical protein [Oryza sa...	-1	97	0.012	2
1	G1073	GI-82091	A25494 hydroxyproline-rich glycoprotein - ...	2	66	0.013	2
1	G1073	GI-170454	cell wall hydroxyproline-rich glycoprotein	2	66	0.013	2
1	G1073	GI-224726	1111324A glycoprotein,Hyp rich [Lycopersic...	2	66	0.013	2
1	G1073	GI-22092	hydroxyproline-rich glycoprotein	2	70	0.013	3
1	G1073	GI-283032	S22456 hydroxyproline-rich glycoprotein - ...	2	70	0.013	3
1	G1073	GI-395147	glycine-rich protein	-1	80	0.015	3
1	G1073	GI-421936	S34666 glycine-rich protein - common tobacco	-1	80	0.015	3
1	G1073	GI-226743	1604369A sulfated surface glycoprotein SSG...	2	74	0.015	3
1	G1073	GI-82698	JQ0985 hydroxyproline-rich glycoprotein pr...	2	70	0.016	3
1	G1073	GI-257041	hydroxyproline-rich glycoprotein, HRGP [ma...	2	70	0.016	3
1	G1073	GI-4007865	Hydroxyproline-rich Glycoprotein (HRGP)	2	70	0.016	3
1	G1073	GI-4755087	aluminum-induced protein; Al-induced protein	-1	95	0.025	1
1	G1073	GI-1184100	pistil extensin-like protein	2	71	0.027	3
1	G1073	GI-21992	extensin	2	72	0.027	3

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1	G1073	GI-81286	S22697 extensin - Volvox carteri (fragment)	2	72	0.027	3
1	G1073	GI-347455	hydroxyproline-rich glycoprotein	2	58	0.034	3
1	G1073	GI-7488674	T07623 extensin homolog HRGP2 - soybean (f...	2	58	0.034	3
1	G1073	GI-2668742	glycine-rich RNA binding protein	-1	89	0.041	1
1	G1073	GI-7439972	T01356 glycine-rich RNA binding protein - ...	-1	89	0.041	1
1	G1073	GI-81870	A29356 hydroxyproline-rich glycoprotein (c...	2	60	0.047	3
1	G1073	GI-7671199	AF246990_1 flagellar autotomy protein Fa1p...	-1	105	0.048	1
1	G1073	GI-2108256	extensin	2	55	0.05	2
1	G1073	GI-600118	extensin-like protein	2	103	0.051	1
1	G1073	GI-1076802	S49915 extensin-like protein - maize	2	103	0.051	1
1	G1073	GI-1096557	2111476A extensin-like domain [Zea mays]	2	103	0.051	1
1	G1073	GI-14253159	VMP3 protein [Volvox carteri f. nagariensis]	2	73	0.055	3
1	G1073	GI-5917664	AF159296_1 extensin-like protein	2	66	0.056	3
1	G1073	GI-12018147	AF309494_1 vegetative cell wall protein gp...	2	67	0.057	3
1	G1073	GI-19322	glycine-rich protein	-1	75	0.058	1
1	G1073	GI-82087	S19774 glycine-rich protein - tomato (frag...	-1	75	0.058	1
1	G1073	GI-1486263	extensin	2	75	0.064	2
1	G1073	GI-7442094	T09964 extensin CYC15 precursor - Madagasc...	2	75	0.064	2
1	G1073	GI-451544	proline-rich cell wall protein	2	74	0.065	2
1	G1073	GI-7441828	T10737 extensin-like cell wall protein - s...	2	74	0.065	2
1	G1073	GI-435039	proline-rich cell wall protein	2	70	0.065	2
1	G1073	GI-7441829	T09854 proline-rich cell wall protein - up...	2	70	0.065	2
1	G1073	GI-496237	homology with RNA-binding proteins in meri...	-1	89	0.08	1
1	G1073	GI-1346181	GRP2_SINAL GLYCINE-RICH RNA-BINDING PROTEI...	-1	89	0.08	1
1	G1073	GI-7440001	T10465 glycine-rich protein 2a - white mus...	-1	89	0.08	1
1	G1073	GI-100687	S20500 hydroxyproline-rich glycoprotein - ...	3	60	0.082	3
1	G1073	GI-433816	hydroxyproline-rich glycoprotein	3	60	0.082	3
1	G1073	GI-100211	S14984 glycine-rich protein (clone uA-3) -...	-1	84	0.089	1
1	G1073	GI-388258	glycine-rich protein	-1	84	0.089	1
1	G1073	GI-347457	hydroxyproline-rich glycoprotein	2	60	0.09	3
1	G1073	GI-2331131	glycine-rich protein	-1	83	0.1	2
1	G1073	GI-20553	precursor polypeptide (aa -27 to 357)	-1	77	0.1	3
1	G1073	GI-82244	A26099 glycine-rich cell wall structural p...	-1	77	0.1	3

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1	G1073	GI-121627	GRP1_PETHY GLYCINE-RICH CELL WALL STRUCTUR...	-1	77	0.1	3
1	G1073	GI-225181	1210313A Gly rich structural protein [Petu...	-1	77	0.1	3
1	G1073	GI-3204132	extensin	2	59	0.11	3
1	G1073	GI-17298137	cold shock protein-1 [Triticum aestivum]	-1	85	0.12	1
1	G1073	GI-81869	C29356 hydroxyproline-rich glycoprotein (c...	2	68	0.12	3
1	G1073	GI-169349	hydroxyproline-rich glycoprotein	2	68	0.12	3
1	G1073	GI-12018149	AF309495_1 gamete-specific hydroxyproline-...	2	59	0.12	3
1	G1073	GI-15866589	hypothetical protein [Capsella rubella]	2	89	0.13	1
1	G1073	GI-20247	glycine-rich cell wall protein	-1	87	0.13	1
1	G1073	GI-72321	KNRZG1 glycine-rich cell wall structural p...	-1	87	0.13	1
1	G1073	GI-121626	GRP1_ORYSA GLYCINE-RICH CELL WALL STRUCTUR...	-1	87	0.13	1
1	G1073	GI-19927	pistil extensin like protein	2	69	0.14	3
1	G1073	GI-322759	PQ0479 pistil extensin-like protein (clone...	2	69	0.14	3
1	G1073	GI-13486631	hypothetical protein [Oryza sativa]	2	68	0.14	2
1	G1073	GI-728594	glycine rich protein, RNA binding protein	-1	81	0.16	2
1	G1073	GI-1076731	S53050 RNA binding protein - barley	-1	81	0.16	2
1	G1073	GI-19917	Pistil extensin like protein, partial CDS...	-2	68	0.16	2
1	G1073	GI-22293	glycine-rich protein	-1	85	0.17	1
1	G1073	GI-82696	S20846 glycine-rich protein - maize	-1	85	0.17	1
1	G1073	GI-13122418	putative glycin-rich protein [Oryza sativa]	-1	79	0.17	3
1	G1073	GI-13161451	putative glycin-rich protein [Oryza sativa]	-1	79	0.17	3
1	G1073	GI-488731	chitinase	2	60	0.17	3
1	G1073	GI-829258	Chitinase	2	60	0.17	3
1	G1073	GI-904359	chitinase 1	2	60	0.17	3
1	G1073	GI-2129478	S51939 chitinase (EC 3.2.1.14) precursor -...	2	60	0.17	3
1	G1073	GI-7488999	S14981 extensin class I (clone w1-8 L) - t...	2	69	0.18	3
1	G1073	GI-2147979	S66275 proline-rich protein - Solanum brev...	2	66	0.18	3
1	G1073	GI-100213	S14972 extensin class I (clone w6) - tomato	2	59	0.21	2
1	G1073	GI-1345536	extensin (class I)	2	59	0.21	2
1	G1073	GI-974605	single-stranded nucleic acid binding protein	-1	84	0.28	1
1	G1073	GI-7439981	S71779 glycine-rich RNA-binding protein GR...	-1	84	0.28	1
1	G1073	GI-2267593	glycine-rich RNA-binding protein	-1	73	0.28	2
1	G1073	GI-7439985	T03583 glycine-rich RNA-binding protein - ...	-1	73	0.28	2

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1	G1073	GI-20420	extensin	2	73	0.29	2
1	G1073	GI-99861	S20790 extensin - almond	2	73	0.29	2
1	G1073	GI-445616	1909363A extensin [Prunus dulcis]	2	73	0.29	2
1	G1073	GI-2624326	OsGRP1	-1	78	0.3	2
1	G1073	GI-7439987	T04346 glycine-rich RNA-binding protein - ...	-1	78	0.3	2
1	G1073	GI-791148	extensin-like protein	2	65	0.32	3
1	G1073	GI-1076556	S54156 extensin-like protein - cowpea (fra...	2	65	0.32	3
1	G1073	GI-18076086	glycine-rich RNA-binding protein [Ricinus ...	-1	83	0.34	1
1	G1073	GI-100753	S13383 hydroxyproline-rich glycoprotein - ...	2	81	0.35	3
1	G1073	GI-228939	1814452D Hyp-rich glycoprotein [Sorghum bi...	2	81	0.35	3
1	G1073	GI-21627	hydroxyproline-rich glycoprotein	2	81	0.35	3
1	G1073	GI-119713	EXTN_SORVU EXTENSIN PRECURSOR (PROLINE-RIC...	2	81	0.35	3
1	G1073	GI-15624033	hypothetical protein [Oryza sativa]	-2	66	0.36	2
1	G1073	GI-100219	S14985 glycine-rich protein (clone uK-4) -...	-1	67	0.36	1
1	G1073	GI-1345534	glycine-rich protein	-1	67	0.36	1
1	G1073	GI-13122430	hypothetical protein [Oryza sativa]	2	68	0.39	2
1	G1073	GI-5726567	AF169205_1 glycine-rich RNA-binding protein	-1	82	0.39	1
1	G1073	GI-21001	GRP 1.0 protein (AA 1 - 252)	-1	81	0.39	2
1	G1073	GI-81867	S01821 glycine-rich protein 1.0 precursor ...	-1	81	0.39	2
1	G1073	GI-121628	GRP1_PHAVU GLYCINE-RICH CELL WALL STRUCTUR...	-1	81	0.39	2
1	G1073	GI-13958149	AF363369_1 acetolactate synthase [Amaranth...	-1	91	0.44	1
1	G1073	GI-13958151	AF363370_1 acetolactate synthase [Amaranth...	-1	91	0.44	1
1	G1073	GI-100216	S14975 extensin class II (clone uJ-2) - to...	2	66	0.44	1
1	G1073	GI-1345538	extensin (class II)	2	66	0.44	1
1	G1073	GI-2108258	extensin	-2	43	0.44	2
1	G1073	GI-17819	glycine-rich RNA binding protein	-1	73	0.45	2
1	G1073	GI-541908	S38331 glycine-rich RNA-binding protein - ...	-1	73	0.45	2
1	G1073	GI-544416	GR10_BRANA GLYCINE-RICH RNA-BINDING PROTEI...	-1	73	0.45	2
1	G1073	GI-4704605	AF109917_1 glycine-rich RNA-binding protein	-1	81	0.45	1
1	G1073	GI-18844875	hypothetical protein [Oryza sativa (japoni...	-1	73	0.45	1
1	G1073	GI-19743	nsGRP-2	-1	84	0.46	1
1	G1073	GI-72323	KNNT2S glycine-rich protein 2 - wood tobacco	-1	84	0.46	1
1	G1073	GI-121631	GRP2_NICSY GLYCINE-RICH CELL WALL STRUCTUR...	-1	84	0.46	1

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1	G1073	GI-322760	PQ0474 pistil extensin-like protein precur...	-2	68	0.47	2
1	G1073	GI-3810890	glycine-rich protein-2	-1	72	0.49	3
1	G1073	GI-19923	pistil extensin like protein, partial CDS	2	67	0.5	2
1	G1073	GI-322758	PQ0477 pistil extensin-like protein (clone...	-2	65	0.52	1
1	G1073	GI-496233	homology with RNA-binding proteins in meri...	-1	81	0.52	1
1	G1073	GI-1346180	GRP1_SINAL GLYCINE-RICH RNA-BINDING PROTEI...	-1	81	0.52	1
1	G1073	GI-7439999	T10463 glycine-rich protein 1a - white mus...	-1	81	0.52	1
1	G1073	GI-21623	glycine-rich RNA-binding protein	-1	79	0.52	1
1	G1073	GI-485420	S12311 glycine-rich RNA-binding protein (c...	-1	79	0.52	1
1	G1073	GI-544421	GRP1_SORVU GLYCINE-RICH RNA-BINDING PROTEIN 1	-1	79	0.52	1
1	G1073	GI-15887008	glycine rich protein [Oryza sativa]	-1	82	0.53	1
1	G1073	GI-169345	hydroxyproline-rich glycoprotein	2	60	0.53	2
1	G1073	GI-18343	put. precursor	2	66	0.53	3
1	G1073	GI-82047	A24354 extensin precursor - carrot	2	66	0.53	3
1	G1073	GI-119711	EXTN_DAUCA EXTENSIN PRECURSOR	2	66	0.53	3
1	G1073	GI-224686	1111211A extensin [Daucus carota]	2	66	0.53	3
1	G1073	GI-17821	glycine-rich_protein_(aa1-291)	-1	79	0.57	2
1	G1073	GI-322647	S31415 glycine-rich protein GRP22 - rape	-1	79	0.57	2
1	G1073	GI-2317764	putative cell wall protein	-1	71	0.58	2
1	G1073	GI-7442070	T07959 probable cell wall protein - loblol...	-1	71	0.58	2
1	G1073	GI-1934994	SGRP-1	-1	80	0.59	1
1	G1073	GI-7439998	T10479 glycine-rich RNA-binding protein GR...	-1	80	0.59	1
1	G1073	GI-1532071	glycine-rich protein	-1	75	0.6	2
1	G1073	GI-7442081	T03371 glycine-rich protein grp3 - maize	-1	75	0.6	2
1	G1073	GI-11692772	AF310674_1 trans-splicing factor Raa3 [Chl...	-1	88	0.6	2
1	G1073	GI-11692774	trans-splicing factor Raa3 [Chlamydomonas ...	-1	88	0.6	2
1	G1073	GI-2674201	glycine-rich RNA-binding protein	-1	80	0.61	1
1	G1073	GI-17932712	putative chitinase [Musa acuminata]	-1	85	0.62	1
1	G1073	GI-791146	extensin-like protein	2	62	0.62	3
1	G1073	GI-7488885	T11671 extensin-like protein 127 - cowpea ...	2	62	0.62	3
1	G1073	GI-99441	A33647 sulfated surface glycoprotein 185 -...	2	80	0.64	2
1	G1073	GI-134920	SSGP_VOLCA SULFATED SURFACE GLYCOPROTEIN 1...	2	80	0.64	2
1	G1073	GI-1405821	SULFATED SURFACE GLYCOPROTEIN 185	2	80	0.64	2

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1	G1073	GI-2226370	RNA-binding protein	-1	75	0.65	2
1	G1073	GI-791150	extensin-like protein	2	57	0.65	3
1	G1073	GI-1076555	S54155 extensin-like protein - cowpea (fra...	2	57	0.65	3
1	G1073	GI-11034630	hypothetical protein [Oryza sativa]	-1	85	0.67	1
1	G1073	GI-14090230	hypothetical protein [Oryza sativa]	-1	85	0.67	1
1	G1073	GI-14488305	AC084884_1 Putative mudrA protein - maize ...	-1	90	0.68	1
1	G1073	GI-15209152	AC091665_11 Putative mudrA protein - maize...	-1	90	0.68	1
1	G1073	GI-7636182	glycine-rich protein [Triticum aestivum]	-1	74	0.68	3
1	G1073	GI-388257	glycine-rich protein	-1	63	0.71	1
1	G1073	GI-399783	GRW1_LYCES GLYCINE-RICH CELL WALL STRUCTUR...	-1	63	0.71	1
1	G1073	GI-1345533	glycine-rich protein	-1	69	0.74	1
1	G1073	GI-7489008	S14980 glycine-rich protein (clone w1-8) -...	-1	69	0.74	1
1	G1073	GI-13486802	hypothetical protein [Oryza sativa]	2	82	0.75	2
1	G1073	GI-20249	gt-2	-1	64	0.75	3
1	G1073	GI-283004	S28030 DNA-binding protein Gt-2 - rice	-1	64	0.75	3
1	G1073	GI-15022163	putative proline-rich protein [Solanum bre...	2	66	0.75	3
1	G1073	GI-18148	glycine-rich protein (AA 1-144) rpt	-1	77	0.76	1
1	G1073	GI-81450	S04069 glycine-rich protein - red goosefoot	-1	77	0.76	1
1	G1073	GI-122785	GRP1_CHERU GLYCINE-RICH PROTEIN HC1	-1	77	0.76	1
1	G1073	GI-486811	S35716 glycine-rich protein (clone DC 9.1)...	-1	77	0.76	1
1	G1073	GI-585219	GRP9_DAUCA GLYCINE-RICH PROTEIN DC9.1	-1	77	0.76	1
1	G1073	GI-4996642	Dof zinc finger protein	-1	66	0.77	2
1	G1073	GI-10799202	glycine-rich RNA-binding protein [Sorghum ...	-1	68	0.78	2
1	G1073	GI-13397640	unnamed protein product [Brassica napus]	2	70	0.78	3
1	G1073	GI-13447449	receptor protein kinase PERK1 [Brassica na...	2	70	0.78	3
1	G1073	GI-19521	proline rich protein	2	65	0.79	3
1	G1073	GI-100248	S16589 proline-rich protein - tomato	2	65	0.79	3
1	G1073	GI-9711862	putative extensin-like protein [Oryza sativa]	2	78	0.79	3
1	G1073	GI-13161443	putative extensin-like protein [Oryza sativa]	2	78	0.79	3
1	G1073	GI-4467884	extensin (class I)	2	62	0.79	1
1	G1073	GI-7488997	S14973 extensin class I (clone uG) - tomat...	2	62	0.79	1
1	G1073	GI-1592792	auxin induced proline rich protein	-2	62	0.79	1
1	G1073	GI-7488752	T09540 proline rich protein, auxin-induced...	-2	62	0.79	1

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1	G1073	GI-7248461	root cap-specific protein [Zea mays]	-1	62	0.79	1
1	G1073	GI-8515090	AF101785_1 putative arabinogalactan protei...	2	66	0.79	3
1	G1073	GI-2950243	extensin	3	68	0.79	2
1	G1073	GI-7446484	T05717 probable extensin - barley (fragment)	3	68	0.79	2
1	G1073	GI-21003	GRP 1.8 protein (AA 1 - 465)	-1	85	0.8	2
1	G1073	GI-81868	S01820 glycine-rich cell wall protein 1.8 ...	-1	85	0.8	2
1	G1073	GI-121632	GRP2_PHAVU GLYCINE-RICH CELL WALL STRUCTUR...	-1	85	0.8	2
1	G1073	GI-3893085	glycine-rich protein 2	-1	80	0.81	1
1	G1073	GI-18461260	hypothetical protein [Oryza sativa]	2	58	0.83	2
1	G1073	GI-18266043	AF458408_1 glycine-rich protein [Brassica ...	-1	74	0.83	1
1	G1073	GI-886961	LMW glutenin	-1	49	0.83	2
1	G1073	GI-1362187	S57645 LMW glutenin precursor - wheat (fra...	-1	49	0.83	2
1	G1073	GI-4115615	root cap-specific glycine-rich protein	-1	79	0.84	1
1	G1073	GI-347453	hydroxyproline-rich glycoprotein	2	67	0.84	2
1	G1073	GI-7488673	T07622 extensin homolog - soybean (fragment)	2	67	0.84	2
1	G1073	GI-19034049	AC092263_11 putative extensin [Oryza sativ...	2	64	0.84	3
1	G1073	GI-5091527	Similar to Zea mays PRP gene.(X60432)	2	71	0.85	2
1	G1073	GI-13365569	hypothetical protein~similar to Oryza sati...	-1	87	0.86	1
1	G1073	GI-1247386	PRP2	2	58	0.86	2
1	G1073	GI-100582	S10334 glycine-rich protein precursor - ba...	-1	79	0.87	1
1	G1073	GI-121644	GRP_HORVU GLYCINE-RICH CELL WALL STRUCTURA...	-1	79	0.87	1
1	G1073	GI-295808	glycine-rich protein	-1	79	0.87	1
1	G1073	GI-2578444	ptxA	2	74	0.87	2
1	G1073	GI-7446483	T06482 probable cell wall protein - garden...	2	74	0.87	2
1	G1073	GI-7442088	T09527 glycine-rich protein 1 - chickpea	-1	76	0.87	1
1	G1073	GI-9988442	hypothetical protein [Oryza sativa]	3	69	0.89	2
1	G1073	GI-10934071	hypothetical protein [Oryza sativa]	3	69	0.89	2
1	G1073	GI-19390	proline rich protein	2	65	0.89	3
1	G1073	GI-100249	S19129 proline-rich protein TPRP-F1 - tomato	2	65	0.89	3
1	G1073	GI-1709767	PRF1_LYCES 36.4 KD PROLINE-RICH PROTEIN	2	65	0.89	3
1	G1073	GI-7211797	AF239615_1 CRANTZ hydroxyproline-rich glyc...	2	61	0.89	3
1	G1073	GI-14140115	putative protein [Oryza sativa]	-1	79	0.9	1
1	G1073	GI-1276958	glycine-rich cell wall protein	-1	56	0.9	2

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1	G1073	GI-7488919	T14302 glycine-rich cell wall protein - ca...	-1	56	0.9	2
1	G1073	GI-13443598	glycine-rich protein 1 [Cicer arietinum]	-1	76	0.9	1
1	G1073	GI-452596	ORF	-1	77	0.9	1
1	G1073	GI-629868	JC2213 hypothetical 14.7K protein, LIM14 -...	-1	77	0.9	1
1	G1073	GI-2653671	120 kDa style glycoprotein	2	66	0.91	2
1	G1073	GI-7489086	T10741 extensin-like protein PRP5 - Persia...	2	66	0.91	2
1	G1073	GI-4105119	dehydrin 10	-1	81	0.91	1
1	G1073	GI-6017946	AF181460_1 dehydrin; DHN10	-1	81	0.91	1
1	G1073	GI-7489009	S14982 glycine-rich protein (clone w10-1) ...	-1	63	0.92	2
1	G1073	GI-397517	hydroxyproline-rich glycoprotein	-2	51	0.93	2
1	G1073	GI-13786451	AC025296_11 putative transcription factor ...	-1	86	0.93	1
1	G1073	GI-81871	B29356 hydroxyproline-rich glycoprotein pr...	2	61	0.93	3
1	G1073	GI-169347	hydroxyproline-rich glycoprotein	2	61	0.93	3
1	G1073	GI-1469223	glycine-rich protein	-1	73	0.93	2
1	G1073	GI-7488554	T14441 glycine-rich protein - wild cabbage...	-1	73	0.93	2
1	G1073	GI-19919	Pistil extensin like protein, partial CDS...	-2	66	0.93	2
1	G1073	GI-322755	PQ0475 pistil extensin-like protein (clone...	-2	66	0.93	2
1	G1073	GI-7024449	glycine-rich protein	-1	73	0.94	1
1	G1073	GI-7024451	glycine-rich RNA-binding protein	-1	76	0.95	1
1	G1073	GI-15623846	putative receptor protein kinase [Oryza sa...	-1	84	0.95	1
1	G1073	GI-1345537	extensin (class I)	2	63	0.96	3
1	G1073	GI-7488998	S14974 extensin class I (clone uG-18) - to...	2	63	0.96	3
1	G1073	GI-7339703	hypothetical protein [Oryza sativa]	2	61	0.96	2
1	G1073	GI-688080	lectin=chitin-binding protein [Solanum tub...	2	59	0.96	1
1	G1073	GI-18844948	hypothetical protein [Oryza sativa (japoni...	3	59	0.96	1
1	G1073	GI-10716605	AC026815_7 putative RNA binding protein [O...	-1	72	0.97	2
1	G1073	GI-1229138	low temperature-responsive RNA-binding pro...	-1	75	0.97	1
1	G1073	GI-7439979	S71453 glycine-rich RNA-binding protein, I...	-1	75	0.97	1
1	G1073	GI-4033606	Extensin	2	61	0.97	3
1	G1073	GI-469072	RNA-binding gricine-rich protein-1 (RGP-1c)	-1	75	0.98	1
1	G1073	GI-2119043	S41773 glycine-rich RNA-binding protein RG...	-1	75	0.98	1
1	G1073	GI-7439982	S59529 RNA-binding glycine-rich protein-1 ...	-1	75	0.98	1
1	G1073	GI-15021756	AF397033_1 nodule extensin [Pisum sativum]	2	53	0.98	2

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1	G1073	GI-1165322	extensin	2	68	0.98	2
1	G1073	GI-7441831	T06782 extensin - soybean	2	68	0.98	2
1	G1073	GI-607771	arabinogalactan-like protein	2	75	0.98	1
1	G1073	GI-1076237	S52994 arabinogalactan-like protein - lobl...	2	75	0.98	1
1	G1073	GI-22550	27kDa storage protein, zein	2	56	0.98	2
1	G1073	GI-100925	S22990 zein, 27K - maize (fragment)	2	56	0.98	2
1	G1073	GI-6063539	hypothetical protein	-1	52	0.98	2
1	G1073	GI-18542888	AC091724_3 Unknown protein [Oryza sativa]	2	56	0.98	2
1	G1073	GI-2852377	hairy root 4	-1	76	0.99	1
1	G1073	GI-7489211	T01982 tumor related protein HR4 - common ...	-1	76	0.99	1
1	G1073	GI-469071	RNA-binding glycine-rich protein-1 (RGP-1b)	-1	67	0.99	2
1	G1073	GI-2119044	S41772 glycine-rich RNA-binding protein RG...	-1	67	0.99	2
1	G1073	GI-17385704	contains EST C73460(E4160)~unknown protein...	-1	79	0.99	1
1	G1073	GI-310925	cysteine-rich extensin-like protein-2	-2	66	0.99	2
1	G1073	GI-539030	B48232 cysteine-rich extensin-like protein...	-2	66	0.99	2
1	G1073	GI-322757	PQ0476 pistil extensin-like protein (clone...	2	60	0.991	2
1	G1073	GI-1076501	S52985 cell wall protein - alfalfa	2	61	0.991	3
1	G1073	GI-3818416	proline-rich cell wall protein	2	61	0.991	3
1	G1073	GI-100214	S14971 extensin class I (clone wY) - tomato	2	57	0.992	2
1	G1073	GI-1345535	extensin (class I)	2	57	0.992	2
1	G1073	GI-18461235	putative nuclear RNA binding protein A [Or...	-1	65	0.992	2
1	G1073	GI-5091598	AC007858_1 10A19I.1	2	75	0.992	1
1	G1073	GI-6911142	putative glycine-rich RNA binding protein 1	-1	72	0.993	1
1	G1073	GI-14164468	hypothetical protein [Oryza sativa]	2	82	0.993	1
1	G1073	GI-13569981	AC079890_1 hypothetical protein [Oryza sat...	2	79	0.993	1
1	G1073	GI-18873840	AC079874_9 unknown protein [Oryza sativa]	2	79	0.993	1
1	G1073	GI-1173628	glycine-rich protein	-1	75	0.995	1
1	G1073	GI-15021742	AF397026_1 nodule extensin [Pisum sativum]	2	56	0.995	3
1	G1073	GI-18103931	glycine rich RNA binding protein [Oryza sa...	-1	75	0.996	1
1	G1073	GI-1345532	glycine-rich protein	-1	57	0.996	1
1	G1073	GI-7489007	S14979 glycine-rich protein (clone uE-7) -...	-1	57	0.996	1
1	G1073	GI-310923	cysteine-rich extensin-like protein-1	-2	66	0.996	2
1	G1073	GI-539029	A48232 cysteine-rich extensin-like protein...	-2	66	0.996	2

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1	G1073	GI-1657851	cold acclimation protein WCOR518	2	67	0.997	2
1	G1073	GI-7446487	T06806 proline rich protein homolog WCOR51...	2	67	0.997	2
1	G1073	GI-7959089	glycine-rich protein [Nicotiana tabacum]	-1	73	0.997	1
1	G1073	GI-8099125	rice EST C27893 corresponds to a region of...	-1	53	0.997	3
1	G1073	GI-18844823	hypothetical protein [Oryza sativa (japoni...	-1	60	0.997	3
1	G1073	GI-6651027	AF127919_1 high mobility group protein I/Y	2	61	0.998	2
1	G1073	GI-727264	hydroxyproline-rich glycoprotein precursor	2	61	0.998	3
1	G1073	GI-7488765	T10863 extensin precursor - kidney bean	2	61	0.998	3
1	G1073	GI-168695	gamma zein	2	56	0.998	2
1	G1073	GI-225315	1211356A zein gamma [Zea mays]	2	56	0.998	2
1	G1073	GI-3126963	acidic chitinase	-1	78	0.998	1
1	G1073	GI-258215	NaPRP3=putative proline-rich protein [Nico...	2	72	0.999	1
1	G1073	GI-322749	JQ1686 extensin-like protein precursor - P...	2	72	0.999	1
1	G1073	GI-1247390	PRP3	2	72	0.999	1
1	G1073	GI-15290188	hypothetical protein [Oryza sativa]	-1	57	0.999	2
1	G1073	GI-15623924	hypothetical protein [Oryza sativa]	-1	57	0.999	2
1	G1073	GI-100209	S25298 extensin (clone Tom J-10) - tomato	2	58	0.999	3
1	G1073	GI-170442	extensin (class I)	2	58	0.999	3
1	G1073	GI-283044	JQ1663 hybrid proline-rich protein - maize	2	73	0.999	2
1	G1073	GI-433707	prolin rich protein	2	73	0.999	2
1	G1073	GI-22313	ABA-inducible gene protein	-1	63	0.999	2
1	G1073	GI-82685	S04536 embryonic abundant protein, glycine...	-1	63	0.999	2
1	G1073	GI-112994	GRPA_MAIZE GLYCINE-RICH RNA-BINDING, ABSCI...	-1	63	0.999	2
1	G1073	GI-226091	1410284A abscisic acid inducible gene [Zea...	-1	63	0.999	2
1	G1073	GI-2598593	MtN12	2	53	0.9991	2
1	G1073	GI-72327	ZMZM5 glutelin 5 - maize	2	56	0.9992	1
1	G1073	GI-15822703	RNA-binding protein precursor [Nicotiana t...	-1	63	0.9992	2
1	G1073	GI-100673	A37288 DNA-binding protein GT-2 - rice (fr...	-1	64	0.9993	2
1	G1073	GI-6016872	EST AU058127(S5254) corresponds to a regio...	2	70	0.9994	1
1	G1073	GI-2196542	glycine-rich protein	-1	74	0.9994	1
1	G1073	GI-7439984	T03442 glycine-rich protein - rice	-1	74	0.9994	1
1	G1073	GI-22289	glutelin-2 precursor	2	56	0.9995	2
1	G1073	GI-22517	zein Zc2	2	56	0.9995	2

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1	G1073	GI-72326	ZMZM19 glutelin 2 precursor (clone pME119)...	2	56	0.9995	2
1	G1073	GI-121472	GLU2_MAIZE GLUTELIN 2 PRECURSOR (ZEIN-GAMM...	2	56	0.9995	2
1	G1073	GI-168485	glutelin-2	2	56	0.9995	2
1	G1073	GI-16305109	27kD gamma zein [Zea mays]	2	56	0.9995	2
1	G1073	GI-2331133	glycine-rich protein	-1	72	0.9997	1
1	G1073	GI-11034632	hypothetical protein [Oryza sativa]	-1	71	0.9998	2
1	G1073	GI-100210	S25299 extensin precursor (clone Tom L-4) ...	2	58	0.9998	3
1	G1073	GI-170444	extensin (class II)	2	58	0.9998	3
1	G1073	GI-12060518	hypothetical protein [Oryza sativa]	-1	63	0.9998	2
1	G1073	GI-1486265	extensin	2	74	0.9999	1
1	G1073	GI-7442095	T09965 extensin CYC17 precursor - Madagasc...	2	74	0.9999	1
1	G1073	GI-15528745	contains ESTs AU093876(E1018),AU093877(E10...	-1	74	0.9999	2
1	G1073	GI-100215	S14970 extensin class I (clone w17-1) - to...	2	53	0.9999	2
1	G1073	GI-1345531	extensin (class I)	2	53	0.9999	2
1	G1073	GI-15289856	hypothetical protein [Oryza sativa]	2	55	0.9999	1
1	G1073	GI-166376	environmental stress-induced protein	-1	55	0.9999	1
1	G1073	GI-7488739	T09610 environmental stress-induced protei...	-1	55	0.9999	1
1	G1073	GI-18813	anther-specific protein SF18	2	64	0.9999	2
1	G1073	GI-100521	S12246 anther-specific protein SF18 precur...	2	64	0.9999	2
1	G1073	GI-114248	ASF1_HELAN ANTHER-SPECIFIC PROTEIN SF18 PR...	2	64	0.9999	2
1	G1073	GI-479021	glycine-rich cell wall protein precursor	-1	64	0.99992	2
1	G1073	GI-1362083	S56703 glycine-rich cell wall protein prec...	-1	64	0.99992	2
1	G1073	GI-469070	RNA-binding glycine-rich protein-1 (RGP-1a)	-1	71	0.99994	1
1	G1073	GI-2119042	S41771 glycine-rich RNA-binding protein RG...	-1	71	0.99994	1
1	G1073	GI-1247388	PRP3	2	68	0.99994	1
1	G1073	GI-13486635	putative protein kinase [Oryza sativa]	2	65	0.99994	3
3	G2789	AL366947	AL366947 MtBA11B10F1 MtBA Medicago truncatul...	1	622	2.70E-58	1
3	G2789	AP003526	AP003526 Oryza sativa chromosome 6 clone P05...	1	628	2.90E-58	1
3	G2789	BM110212	BM110212 EST557748 potato roots Solanum tube...	1	617	6.10E-58	1
3	G2789	BG647144	BG647144 EST508763 HOGA Medicago truncatula ...	1	614	1.20E-57	1
3	G2789	AW774484	AW774484 EST333635 KV3 Medicago truncatula c...	1	611	2.70E-57	1
3	G2789	BH664974	BH664974 BOMBC11TF BO_2_3_KB Brassica olerac...	2	540	2.90E-57	2
3	G2789	AW574000	AW574000 EST316591 GVN Medicago truncatula c...	1	610	3.50E-57	1

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3	G2789	BG134451	BG134451 EST467343 tomato crown gall Lycoper...	1	588	9.70E-55	1
3	G2789	BH566718	BH566718 BOHCV23TR BOHC Brassica oleracea ge...	-2	584	1.80E-54	1
3	G2789	OSJN00182	AL662981 Oryza sativa chromosome 4 clone OSJ...	1	592	1.90E-54	1
3	G2789	AW349284	AW349284 GM210004B21H7 Gm-r1021 Glycine max ...	-2	500	2.00E-54	2
3	G2789	BG581882	BG581882 EST483618 GVN Medicago truncatula c...	3	580	4.80E-54	1
3	G2789	AW350603	AW350603 GM210008B10B12 Gm-r1021 Glycine max...	-1	565	1.90E-52	1
3	G2789	BH729110	BH729110 BOHVN82TF BO_2_3_KB Brassica olerac...	-2	564	2.60E-52	1
3	G2789	AP004165	AP004165 Oryza sativa chromosome 2 clone OJ1...	-3	570	4.10E-52	1
3	G2789	AP004020	AP004020 Oryza sativa chromosome 2 clone OJ1...	2	568	6.70E-52	1
3	G2789	AP003891	AP003891 Oryza sativa chromosome 8 clone OJ1...	2	564	1.80E-51	1
3	G2789	AP004587	AP004587 Oryza sativa chromosome 8 clone P05...	3	564	1.80E-51	1
3	G2789	BG583651	BG583651 EST485403 GVN Medicago truncatula c...	3	269	2.20E-51	3
3	G2789	BE203784	BE203784 EST396460 KV0 Medicago truncatula c...	2	546	3.30E-50	1
3	G2789	AW980581	AW980581 EST391734 GVN Medicago truncatula c...	3	542	6.30E-50	1
3	G2789	AP004635	AP004635 Oryza sativa chromosome 8 clone P06...	-2	547	1.10E-49	1
3	G2789	AP004698	AP004698 Oryza sativa chromosome 8 clone P04...	2	547	1.10E-49	1
3	G2789	BF067277	BF067277 st37f11.y1 Gm-c1067 Glycine max cDN...	3	527	3.80E-48	1
3	G2789	BH730050	BH730050 BOMEB22TF BO_2_3_KB Brassica olerac...	-1	522	6.20E-48	1
3	G2789	BF254863	BF254863 HVSMEf0005E05f Hordeum vulgare seed...	2	516	3.70E-47	1
3	G2789	AP004757	AP004757 Oryza sativa chromosome 6 clone P06...	-3	521	6.40E-47	1
3	G2789	BH685875	BH685875 BOMBO90TR BO_2_3_KB Brassica olerac...	-1	510	1.50E-46	1
3	G2789	BH550632	BH550632 BOGUC18TR BOGU Brassica oleracea ge...	-2	507	2.30E-46	1
3	G2789	BH660108	BH660108 BOHVI48TF BO_2_3_KB Brassica olerac...	-1	503	6.40E-46	1
3	G2789	BH419879	BH419879 BOGGX69TF BOGG Brassica oleracea ge...	-2	499	1.80E-45	1
3	G2789	BH596283	BH596283 BOGBL42TR BOGB Brassica oleracea ge...	2	498	2.40E-45	1
3	G2789	AW776082	AW776082 EST335147 DSIL Medicago truncatula ...	3	494	8.20E-45	1
3	G2789	BH669958	BH669958 BOMEJ12TF BO_2_3_KB Brassica olerac...	1	495	9.10E-45	1
3	G2789	BI321563	BI321563 saf12g07.y3 Gm-c1076 Glycine max cD...	1	488	3.70E-44	1
3	G2789	BH459056	BH459056 BOGKX90TR BOGK Brassica oleracea ge...	-2	483	9.10E-44	1
3	G2789	BI701170	BI701170 sag55e11.y1 Gm-c1082 Glycine max cD...	2	476	6.60E-43	1
3	G2789	BH481983	BH481983 BOGYI73TR BOGY Brassica oleracea ge...	2	471	1.70E-42	1
3	G2789	BH513264	BH513264 BOHQC93TR BOHQ Brassica oleracea ge...	-3	470	2.10E-42	1
3	G2789	AW560824	AW560824 EST315872 DSIR Medicago truncatula ...	2	471	2.40E-42	1

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3	G2789	BH717588	BH717588 BOMDB19TF BO_2_3_KB Brassica olerac...	2	470	2.70E-42	1
3	G2789	BG583687	BG583687 EST485440 GVN Medicago truncatula c...	2	464	9.60E-42	1
3	G2789	BF004270	BF004270 EST432768 KV1 Medicago truncatula c...	3	464	1.60E-41	1
3	G2789	BE999313	BE999313 EST431036 GVSN Medicago truncatula ...	1	385	1.70E-41	2
3	G2789	BH550963	BH550963 BOHQE85TR BOHQ Brassica oleracea ge...	-3	460	2.30E-41	1
3	G2789	AW720668	AW720668 LjNEST14h9rc Lotus japonicus nodule...	1	461	2.40E-41	1
3	G2789	BH688757	BH688757 BOMDL66TF BO_2_3_KB Brassica olerac...	2	461	2.40E-41	1
3	G2789	BI419871	BI419871 LjNEST17a9r Lotus japonicus nodule ...	2	454	2.00E-40	1
3	G2789	BH419964	BH419964 BOGQI28TF BOGQ Brassica oleracea ge...	-1	453	2.30E-40	1
3	G2789	AW774872	AW774872 EST334023 KV3 Medicago truncatula c...	3	446	1.50E-39	1
3	G2789	BM526396	BM526396 sal40g01.y1 Gm-c1059 Glycine max cD...	3	441	3.70E-39	1
3	G2789	BM779718	BM779718 EST590294 KV2 Medicago truncatula c...	-3	432	2.20E-38	1
3	G2789	BG599840	BG599840 EST504735 cSTS Solanum tuberosum cD...	3	258	5.20E-38	2
3	G2789	AP004680	AP004680 Oryza sativa chromosome 6 clone OSJ...	-2	263	9.70E-38	2
3	G2789	BG881387	BG881387 sae81e03.y1 Gm-c1065 Glycine max cD...	3	427	1.10E-37	1
3	G2789	AV422634	AV422634 AV422634 Lotus japonicus young plan...	3	425	2.20E-37	1
3	G2789	BG646893	BG646893 EST508512 HOGA Medicago truncatula ...	2	419	5.90E-37	1
3	G2789	BM523502	BM523502 sam84f06.y2 Gm-c1087 Glycine max cD...	1	410	6.50E-36	1
3	G2789	BE998262	BE998262 EST429985 GVSN Medicago truncatula ...	2	405	2.40E-35	1
3	G2789	AW621455	AW621455 EST312253 tomato root during/after ...	2	391	5.70E-34	1
3	G2789	AW349908	AW349908 GM210006A20F9 Gm-r1021 Glycine max ...	-3	389	1.00E-33	1
3	G2789	AW780525	AW780525 sl72a07.y1 Gm-c1027 Glycine max cDN...	1	381	1.20E-32	1
3	G2789	AP003683	AP003683 Oryza sativa genomic DNA, chromosom...	3	383	2.70E-32	1
3	G2789	AV415346	AV415346 AV415346 Lotus japonicus young plan...	3	369	2.10E-31	1
3	G2789	AI736668	AI736668 sb32a03.y1 Gm-c1012 Glycine max cDN...	2	362	7.90E-31	1
3	G2789	AP003938	AP003938 Oryza sativa chromosome 6 clone OJ1...	-2	365	2.20E-30	1
3	G2789	BI426899	BI426899 sag08g12.y1 Gm-c1080 Glycine max cD...	1	355	4.40E-30	1
3	G2789	BG647027	BG647027 EST508646 HOGA Medicago truncatula ...	3	349	1.30E-29	1
3	G2789	BJ203193	BJ203193 BJ203193 normalized full length cDN...	1	234	1.50E-29	2
3	G2789	AW648634	AW648634 EST327184 tomato germinating seedli...	3	346	4.10E-29	1
3	G2789	AP004319	AP004319 Oryza sativa chromosome 1 clone B10...	1	207	4.20E-29	2
3	G2789	BH439306	BH439306 BOHGL38TR BOHG Brassica oleracea ge...	1	346	4.30E-29	1
3	G2789	BH430946	BH430946 BOHSM94TF BOHS Brassica oleracea ge...	-1	344	5.50E-29	1

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3	G2789	BH679922	BH679922 BOMNO92TR BO_2_3_KB Brassica olerac...	3	343	6.00E-29	1
3	G2789	BI308126	BI308126 EST529536 GPOD Medicago truncatula ...	3	344	6.10E-29	1
3	G2789	BE020549	BE020549 sm45a11.y1 Gm-c1028 Glycine max cDN...	3	346	6.80E-29	1
3	G2789	BH491363	BH491363 BOGPS71TR BOGP Brassica oleracea ge...	-1	339	1.60E-28	1
3	G2789	AI494847	AI494847 sb06b09.y1 Gm-c1004 Glycine max cDN...	1	341	1.70E-28	1
3	G2789	BF650426	BF650426 NF096G12EC1F1098 Elicited cell cult...	3	337	3.20E-28	1
3	G2789	BG600318	BG600318 EST505213 cSTS Solanum tuberosum cD...	1	337	7.00E-28	1
3	G2789	BH173434	BH173434 0104B13 maize genomic ORF library F...	-1	332	2.20E-27	1
3	G2789	BI970749	BI970749 GM830011A20H08 Gm-r1083 Glycine max...	-1	327	3.30E-27	1
3	G2789	AP004303	AP004303 Oryza sativa chromosome 7 clone P04...	2	334	4.20E-27	1
3	G2789	BM525692	BM525692 sak62d03.y1 Gm-c1036 Glycine max cD...	1	325	6.80E-27	1
3	G2789	AI522924	AI522924 sa92b03.y1 Gm-c1004 Glycine max cDN...	2	326	6.80E-27	1
3	G2789	BG644865	BG644865 EST506484 KV3 Medicago truncatula c...	2	323	7.90E-27	1
3	G2789	AW348874	AW348874 GM210010A10G1 Gm-r1021 Glycine max ...	-2	322	1.10E-26	1
3	G2789	BE496294	BE496294 NXCI_022_C11_F NXCI (Nsf Xylem Comp...	1	323	1.30E-26	1
3	G2789	BI786439	BI786439 sai49b05.y1 Gm-c1065 Glycine max cD...	1	322	1.50E-26	1
3	G2789	BE442709	BE442709 WHE1105_B09_C17ZS Wheat etiolated s...	3	314	1.00E-25	1
3	G2789	BE445433	BE445433 WHE1136_A09_B18ZS Wheat etiolated s...	2	314	1.00E-25	1
3	G2789	BM371214	BM371214 EBro04_SQ003_M20_R IGF Barley EBro0...	2	314	1.50E-25	1
3	G2789	BJ189956	BJ189956 BJ189956 normalized full length cDN...	3	310	2.50E-25	1
3	G2789	BE442615	BE442615 WHE1101_G09_M17ZS Wheat etiolated s...	2	306	7.40E-25	1
3	G2789	BM407572	BM407572 EST581899 potato roots Solanum tube...	1	220	7.50E-25	2
3	G2789	BI699513	BI699513 sag37g08.y1 Gm-c1081 Glycine max cD...	2	304	1.30E-24	1
3	G2789	BF588135	BF588135 FM1_38_B09.b1_A003 Floral-Induced M...	3	302	2.00E-24	1
3	G2789	BH732637	BH732637 BOMBI03TF BO_2_3_KB Brassica olerac...	2	300	2.50E-24	1
3	G2789	BI971972	BI971972 sag84f09.y1 Gm-c1084 Glycine max cD...	1	300	3.30E-24	1
3	G2789	AW596625	AW596625 sj14f10.y1 Gm-c1032 Glycine max cDN...	2	299	4.10E-24	1
3	G2789	BE342838	BE342838 EST395682 potato stolon, Cornell Un...	1	295	9.70E-24	1
3	G2789	BI924382	BI924382 EST544271 tomato flower, buds 0-3 m...	3	295	1.20E-23	1
3	G2789	BE432188	BE432188 EST398717 tomato breaker fruit, TIG...	3	292	2.40E-23	1
3	G2789	BH480897	BH480897 BOGRA01TF BOGR Brassica oleracea.ge...	-1	289	4.30E-23	1
3	G2789	BH588550	BH588550 BOHOI48TR BOHO Brassica oleracea ge...	-2	286	8.20E-23	1
3	G2789	AV424890	AV424890 AV424890 Lotus japonicus young plan...	3	284	2.00E-22	1

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3	G2789	BG045781	BG045781 saa06a11.y1 Gm-c1058 Glycine max cD...	3	281	5.40E-22	1
3	G2789	AL373204	AL373204 MtBA56C11F1 MtBA Medicago truncatul...	3	277	1.00E-21	1
3	G2789	AW099294	AW099294 sd37h01.y1 Gm-c1016 Glycine max cDN...	2	277	1.70E-21	1
3	G2789	BG465540	BG465540 RHIZ2_45_G09.b1_A003 Rhizome2 (RHIZ...	3	267	1.00E-20	1
3	G2789	BE444180	BE444180 WHE1128_B06_D12ZS Wheat etiolated s...	2	266	1.40E-20	1
3	G2789	AW672482	AW672482 LG1_360_E08.b1_A002 Light Grown 1 (...	3	264	2.00E-20	1
3	G2789	BI406306	BI406306 159E11 Mature tuber lambda ZAP Sola...	1	262	3.20E-20	1
3	G2789	BI929403	BI929403 EST549292 tomato flower, 3 - 8 mm b...	1	259	4.70E-20	1
3	G2789	AW596434	AW596434 sj12d05.y1 Gm-c1032 Glycine max cDN...	2	260	7.80E-20	1
3	G2789	AW776953	AW776953 EST336018 DSIL Medicago truncatula ...	2	256	1.30E-19	1
3	G2789	BG593477	BG593477 EST492155 cSTS Solanum tuberosum cD...	3	256	1.40E-19	1
3	G2789	BG350206	BG350206 084D10 Mature tuber lambda ZAP Sola...	3	255	1.40E-19	1
3	G2789	BE587763	BE587763 WHE0652_C06_E12ZM Secale cereale ro...	1	256	1.60E-19	1
3	G2789	BI074657	BI074657 IP1_14_F04.b1_A002 Immature pannicl...	1	253	2.80E-19	1
3	G2789	BG596340	BG596340 EST495018 cSTS Solanum tuberosum cD...	3	249	6.60E-19	1
3	G2789	BM322182	BM322182 PIC1_1_A05.b1_A002 Pathogen-infecte...	2	249	7.10E-19	1
3	G2789	BM322317	BM322317 PIC1_3_A06.b1_A002 Pathogen-infecte...	2	249	7.20E-19	1
3	G2789	BM322320	BM322320 PIC1_3_A09.b1_A002 Pathogen-infecte...	2	249	7.50E-19	1
3	G2789	BM322319	BM322319 PIC1_3_A08.b1_A002 Pathogen-infecte...	2	249	8.00E-19	1
3	G2789	BE822274	BE822274 GM700017A10A4 Gm-r1070 Glycine max ...	-1	247	9.30E-19	1
3	G2789	BM322185	BM322185 PIC1_1_A08.b1_A002 Pathogen-infecte...	2	249	9.60E-19	1
3	G2789	BM322192	BM322192 PIC1_1_B08.b1_A002 Pathogen-infecte...	2	249	9.60E-19	1
3	G2789	BM322318	BM322318 PIC1_3_A07.b1_A002 Pathogen-infecte...	2	249	9.60E-19	1
3	G2789	AW979681	AW979681 EST341290 tomato root deficiency, C...	1	247	1.30E-18	1
3	G2789	AP003074	AP003074 Oryza sativa genomic DNA, chromosom...	-1	254	1.30E-18	1
3	G2789	AC007789	AC007789 Oryza sativa BAC OSJNBa0049B20 geno...	-1	254	1.30E-18	1
3	G2789	AV933535	AV933535 AV933535 K. Sato unpublished cDNA l...	1	246	1.40E-18	1
3	G2789	BI321153	BI321153 saf48b01.y3 Gm-c1077 Glycine max cD...	1	245	1.90E-18	1
3	G2789	AI522913	AI522913 sa91h08.y1 Gm-c1004 Glycine max cDN...	1	246	2.00E-18	1
3	G2789	BH596271	BH596271 BOGBL42TF BOGB Brassica oleracea ge...	-3	243	2.50E-18	1
3	G2789	BF324870	BF324870 su17c07.y1 Gm-c1066 Glycine max cDN...	1	245	2.50E-18	1
3	G2789	AW622329	AW622329 EST313127 tomato root during/after ...	2	243	3.90E-18	1
3	G2789	BI139442	BI139442 F131P74Y Populus flower cDNA librar...	-1	242	4.60E-18	1

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3	G2789	BE496149	BE496149 WHE1262_H03_P06ZS Secale cereale an...	2	241	6.70E-18	1
3	G2789	BM322184	BM322184 PIC1_1_A07.b1_A002 Pathogen-infecte...	2	241	8.20E-18	1
3	G2789	BG583795	BG583795 EST485550 GVN Medicago truncatula c...	1	238	8.60E-18	1
3	G2789	BI972076	BI972076 sag85g11.y1 Gm-c1084 Glycine max cD...	2	239	9.00E-18	1
3	G2789	BG441060	BG441060 GA__Ea0011I19f Gossypium arboreum 7...	3	237	9.50E-18	1
3	G2789	BF429428	BF429428 WHE1803_A09_B17ZS Secale cereale an...	1	239	1.20E-17	1
3	G2789	AP003917	AP003917 Oryza sativa chromosome 8 clone OJ1...	3	181	1.20E-17	2
3	G2789	BH650598	BH650598 BOHZR58TR BO_2_3_KB Brassica olerac...	1	237	1.30E-17	1
3	G2789	AV917319	AV917319 AV917319 K. Sato unpublished cDNA l...	2	236	1.60E-17	1
3	G2789	AW455702	AW455702 707090A08.x1 707 - Mixed adult tiss...	3	234	2.90E-17	1
3	G2789	BI788210	BI788210 sag68a10.y1 Gm-c1082 Glycine max cD...	3	234	3.00E-17	1
3	G2789	BI699401	BI699401 sag36e12.y1 Gm-c1081 Glycine max cD...	1	235	3.10E-17	1
3	G2789	AMA132349	AJ132349 Antirrhinum majus mRNA for SAP1 pro...	3	233	3.50E-17	1
3	G2789	BE555817	BE555817 sp94c01.y1 Gm-c1045 Glycine max cDN...	3	232	5.30E-17	1
3	G2789	BE330349	BE330349 so77e09.y1 Gm-c1040 Glycine max cDN...	3	232	5.40E-17	1
3	G2789	AW755604	AW755604 sl05h07.y1 Gm-c1036 Glycine max cDN...	3	231	6.00E-17	1
3	G2789	AL372048	AL372048 MtBA48C06F1 MtBA Medicago truncatul...	1	232	7.60E-17	1
3	G2789	BG589060	BG589060 EST490869 MHRP- Medicago truncatula...	1	228	1.00E-16	1
3	G2789	BI929489	BI929489 EST549378 tomato flower, 3 - 8 mm b...	1	175	1.10E-16	2
3	G2789	BE357932	BE357932 DG1_23_D12.b1_A002 Dark Grown 1 (DG...	1	228	1.30E-16	1
3	G2789	AV422959	AV422959 AV422959 Lotus japonicus young plan...	2	229	1.30E-16	1
3	G2789	BE600816	BE600816 PI1_90_E07.b1_A002 Pathogen induced...	3	228	1.30E-16	1
3	G2789	BG241750	BG241750 RHIZ2_50_G05.b1_A003 Rhizome2 (RHIZ...	3	228	1.60E-16	1
3	G2789	BI974724	BI974724 sai72b06.y1 Gm-c1068 Glycine max cD...	1	227	1.70E-16	1
3	G2789	BE125776	BE125776 DG1_57_B07.b1_A002 Dark Grown 1 (DG...	1	228	1.80E-16	1
3	G2789	BG909764	BG909764 TaLr1108d02R TaLr1 Triticum aestivu...	3	227	1.80E-16	1
3	G2789	BI266587	BI266587 NF099D09IN1F1078 Insect herbivory M...	2	226	1.90E-16	1
3	G2789	AI965992	AI965992 sc25a12.y1 Gm-c1013 Glycine max cDN...	3	225	2.60E-16	1
3	G2789	BE591277	BE591277 WHE1655-1658_J17_J17ZS Wheat heat s...	1	225	2.70E-16	1
3	G2789	BI946361	BI946361 01104 leafy spurge Lambda HybriZAP ...	1	223	4.10E-16	1
3	G2789	AV411735	AV411735 AV411735 Lotus japonicus young plan...	1	224	4.50E-16	1
3	G2789	BF587149	BF587149 FM1_32_G07.b1_A003 Floral-Induced M...	3	223	5.70E-16	1
3	G2789	BE609898	BE609898 sq46e12.y1 Gm-c1019 Glycine max cDN...	3	220	9.40E-16	1

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3	G2789	AW310124	AW310124 sf31d10.x1 Gm-c1028 Glycine max cDN...	-1	219	1.00E-15	1
3	G2789	PSDBLPPD1	X98739 P.sativum mRNA encoding DNA-binding P...	1	221	1.50E-15	1
3	G2789	PSDBPPD1	X98738 P.sativum mRNA encoding DNA-binding p...	1	221	2.00E-15	1
3	G2789	AW755831	AW755831 sl09h02.y1 Gm-c1036 Glycine max cDN...	3	218	2.10E-15	1
3	G2789	AW278127	AW278127 sf40a09.y1 Gm-c1009 Glycine max cDN...	1	217	2.20E-15	1
3	G2789	BE643892	BE643892 NXCI_048_F12_F NXCI (Nsf Xylem Comp...	3	217	2.60E-15	1
3	G2789	D42950	D42950 D42950 Rice callus cDNA (H.Uchimiya) ...	2	217	2.70E-15	1
3	G2789	BG651836	BG651836 sad61f05.y1 Gm-c1051 Glycine max cD...	3	216	2.90E-15	1
3	G2789	AW906401	AW906401 EST342523 potato stolon, Cornell Un...	2	215	3.60E-15	1
3	G2789	AW066510	AW066510 660015F03.y1 660 - Mixed stages of ...	1	213	5.90E-15	1
3	G2789	AI881841	AI881841 606074A03.y1 606 - Ear tissue cDNA ...	3	211	7.70E-15	1
3	G2789	BE807468	BE807468 ss22h03.y1 Gm-c1047 Glycine max cDN...	2	211	1.20E-14	1
3	G2789	BE586257	BE586257 WHE501_B07_C13ZR Secale cereale alu...	2	209	1.30E-14	1
3	G2789	BF637181	BF637181 NF050F02LF1F1016 Developing leaf Me...	3	209	1.30E-14	1
3	G2789	BE600623	BE600623 PI1_89_D08.b1_A002 Pathogen induced...	3	208	2.00E-14	1
3	G2789	AW928863	AW928863 EST337651 tomato flower buds 8 mm t...	3	206	2.90E-14	1
3	G2789	BM358644	BM358644 GA__Ea0011I19r Gossypium arboreum 7...	3	205	3.20E-14	1
3	G2789	BG043009	BG043009 st91a08.y1 Gm-c1054 Glycine max cDN...	3	206	4.60E-14	1
3	G2789	BG130143	BG130143 EST475789 tomato shoot/meristem Lyc...	1	202	6.10E-14	1
3	G2789	AW309814	AW309814 sf25b03.x1 Gm-c1028 Glycine max cDN...	-1	202	6.10E-14	1
3	G2789	BH677454	BH677454 BOHZJ50TR BO_2_3_KB Brassica olerac...	-3	201	6.40E-14	1
3	G2789	AI960613	AI960613 sc86h10.y1 Gm-c1018 Glycine max cDN...	1	203	6.90E-14	1
3	G2789	BM086350	BM086350 sah38h08.y1 Gm-c1036 Glycine max cD...	3	201	9.50E-14	1
3	G2789	BG888793	BG888793 EST514644 cSTD Solanum tuberosum cD...	3	199	1.10E-13	1
3	G2789	BI932139	BI932139 EST552028 tomato flower, 8 mm to pr...	1	199	1.10E-13	1
3	G2789	BG132224	BG132224 EST465116 tomato crown gall Lycoper...	2	200	1.40E-13	1
3	G2789	BG599554	BG599554 EST504449 cSTS Solanum tuberosum cD...	2	198	1.50E-13	1
3	G2789	BM307331	BM307331 sak27h05.y1 Gm-c1075 Glycine max cD...	1	199	1.60E-13	1
3	G2789	BM427899	BM427899 NXRV_006_A04_F NXRV (Nsf Xylem Root...	1	199	1.80E-13	1
3	G2789	BM094106	BM094106 sah25e06.y1 Gm-c1036 Glycine max cD...	1	198	2.20E-13	1
3	G2789	BH510717	BH510717 BOGGW07TF BOGG Brassica oleracea ge...	1	197	2.20E-13	1
3	G2789	AI988292	AI988292 sc98f12.y1 Gm-c1020 Glycine max cDN...	2	196	3.10E-13	1
3	G2789	BE345655	BE345655 946021H10.y2 946 - tassel primordiu...	3	196	3.30E-13	1

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3	G2789	BF257835	BF257835 HVSMEf0014A01f Hordeum vulgare seed...	2	195	4.00E-13	1
3	G2789	BG352828	BG352828 sab91g04.y1 Gm-c1040 Glycine max cD...	3	194	5.90E-13	1
3	G2789	AW773742	AW773742 EST332728 KV3 Medicago truncatula c...	3	192	8.10E-13	1
3	G2789	BI943944	BI943944 sa62b04.y1 Gm-c1004 Glycine max cDN...	2	191	1.40E-12	1
3	G2789	BI096714	BI096714 949019H11.y1 949 - Juvenile leaf an...	2	190	1.50E-12	1
3	G2789	BJ186205	BJ186205 BJ186205 normalized full length cDN...	1	189	1.70E-12	1
3	G2789	BI700385	BI700385 sag60b11.y1 Gm-c1082 Glycine max cD...	2	190	1.80E-12	1
3	G2789	BI270829	BI270829 NF002D02FL1F1026 Developing flower ...	1	190	1.80E-12	1
3	G2789	BF625927	BF625927 HVSMEa0014H11f Hordeum vulgare seed...	1	189	2.10E-12	1
3	G2789	BE202989	BE202989 EST403011 KV1 Medicago truncatula c...	-3	188	2.40E-12	1
3	G2789	AI443215	AI443215 sa45h07.y1 Gm-c1004 Glycine max cDN...	1	187	4.10E-12	1
3	G2789	BM079070	BM079070 MEST88-H11.T3 ISUM4-TN Zea mays cDN...	-1	182	7.50E-12	1
3	G2789	BG662369	BG662369 Ljirnpest43-456-c2 Ljirnp Lambda Hy...	1	187	1.00E-11	1
3	G2789	BM094108	BM094108 sah25e08.y1 Gm-c1036 Glycine max cD...	1	182	1.10E-11	1
3	G2789	BG592977	BG592977 EST491655 cSTS Solanum tuberosum cD...	-2	180	1.50E-11	1
3	G2789	BE805340	BE805340 ss41d08.y1 Gm-c1061 Glycine max cDN...	1	181	1.80E-11	1
3	G2789	BI469296	BI469296 sai10a11.y1 Gm-c1053 Glycine max cD...	3	179	2.50E-11	1
3	G2789	AW773741	AW773741 EST332727 KV3 Medicago truncatula c...	3	176	4.20E-11	1
3	G2789	BJ158045	BJ158045 BJ158045 full length cDNA library, ...	-3	176	4.40E-11	1
3	G2789	BI931107	BI931107 EST550996 tomato flower, 8 mm to pr...	1	175	4.60E-11	1
3	G2789	BM521838	BM521838 sak76f11.y1 Gm-c1036 Glycine max cD...	2	175	5.30E-11	1
3	G2789	BM524672	BM524672 sal18d07.y1 Gm-c1059 Glycine max cD...	2	174	6.80E-11	1
3	G2789	BM524654	BM524654 sal18b12.y1 Gm-c1059 Glycine max cD...	2	174	7.20E-11	1
3	G2789	BG240061	BG240061 OV1_17_D10.b1_A002 Ovary 1 (OV1) So...	1	173	9.00E-11	1
3	G2789	BG240043	BG240043 OV1_17_B12.b1_A002 Ovary 1 (OV1) So...	1	173	9.30E-11	1
3	G2789	BM136003	BM136003 WHE2604_D04_H08ZS Wheat Fusarium gr...	-1	172	1.00E-10	1
3	G2789	BE996884	BE996884 NXCI_103_F12_F NXCI (Nsf Xylem Comp...	1	174	1.20E-10	1
3	G2789	BG240220	BG240220 OV1_19_D02.b1_A002 Ovary 1 (OV1) So...	1	173	1.20E-10	1
3	G2789	BF112609	BF112609 EST440199 tomato breaker fruit Lyco...	3	172	1.30E-10	1
3	G2789	AW761430	AW761430 sl67d09.y1 Gm-c1027 Glycine max cDN...	2	172	1.50E-10	1
3	G2789	BI927526	BI927526 EST547415 tomato flower, 3 - 8 mm b...	3	169	2.00E-10	1
3	G2789	BI435896	BI435896 EST538657 P. infestans-challenged l...	3	171	2.30E-10	1
3	G2789	BE639390	BE639390 946024E11.y1 946 - tassel primordiu...	1	168	3.00E-10	1

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3	G2789	AI897688	AI897688 EST267131 tomato ovary, TAMU Lycope...	3	168	3.70E-10	1
3	G2789	BI267267	BI267267 NF100C06IN1F1070 Insect herbivory M...	2	114	4.70E-10	2
3	G2789	BI928278	BI928278 EST548167 tomato flower, 3 - 8 mm b...	1	175	5.60E-10	1
3	G2789	BF636643	BF636643 NF091G07DT1F1055 Drought Medicago t...	1	166	6.70E-10	1
3	G2789	AI487942	AI487942 EST246264 tomato ovary, TAMU Lycope...	1	167	9.40E-10	1
3	G2789	BG040551	BG040551 NXSI_112_D08_F NXSI (Nsf Xylem Side...	1	165	1.00E-09	1
3	G2789	BE587194	BE587194 WHE0519_B07_D13ZR Secale cereale al...	1	165	1.40E-09	1
3	G2789	AV411140	AV411140 AV411140 Lotus japonicus young plan...	2	162	2.30E-09	1
3	G2789	AW720136	AW720136 LjNEST14h9r Lotus japonicus nodule ...	1	162	2.50E-09	1
3	G2789	BE923621	BE923621 EST427390 potato leaves and petiole...	1	160	3.60E-09	1
3	G2789	AW225998	AW225998 ST76B07 Pine TriplEx shoot tip libr...	2	158	6.10E-09	1
3	G2789	BG582457	BG582457 EST484202 GVN Medicago truncatula c...	3	158	7.90E-09	1
3	G2789	HVU234403	AJ234403 Hordeum vulgare partial mRNA; clone...	1	156	8.50E-09	1
3	G2789	AV425818	AV425818 AV425818 Lotus japonicus young plan...	3	157	9.50E-09	1
3	G2789	AW031261	AW031261 EST274636 tomato callus, TAMU Lycop...	1	155	1.00E-08	1
3	G2789	BG594217	BG594217 EST492895 cSTS Solanum tuberosum cD...	2	155	1.10E-08	1
3	G2789	BG239709	BG239709 sab74e11.y1 Gm-c1032 Glycine max cD...	3	155	1.10E-08	1
3	G2789	BF187248	BF187248 EST443535 potato stolon, Cornell Un...	2	155	1.30E-08	1
3	G2789	AU198263	AU198263 AU198263 Rice green shoot Oryza sat...	1	155	1.40E-08	1
3	G2789	BI972355	BI972355 sag90d06.y1 Gm-c1084 Glycine max cD...	2	154	1.60E-08	1
3	G2789	AW760534	AW760534 sl51e09.y1 Gm-c1027 Glycine max cDN...	1	153	1.90E-08	1
3	G2789	BJ196157	BJ196157 BJ196157 normalized full length cDN...	1	153	3.90E-08	1
3	G2789	AV410107	AV410107 AV410107 Lotus japonicus young plan...	2	152	4.10E-08	1
3	G2789	BM309583	BM309583 sak64c09.y1 Gm-c1036 Glycine max cD...	1	150	4.30E-08	1
3	G2789	AW776126	AW776126 EST335191 DSIL Medicago truncatula ...	2	158	1.30E-07	1
3	G2789	BE446692	BE446692 WHE1139_D09_H17ZS Wheat etiolated s...	2	147	1.30E-07	1
3	G2789	BE923864	BE923864 EST427633 potato leaves and petiole...	1	146	1.70E-07	1
3	G2789	AW132605	AW132605 se06d10.y1 Gm-c1013 Glycine max cDN...	3	144	2.30E-07	1
3	G2789	AV423934	AV423934 AV423934 Lotus japonicus young plan...	3	145	2.30E-07	1
3	G2789	BI788421	BI788421 sag70e10.y1 Gm-c1082 Glycine max cD...	3	143	3.40E-07	1
3	G2789	BM405827	BM405827 EST580154 potato roots Solanum tube...	2	143	3.90E-07	1
3	G2789	AV421337	AV421337 AV421337 Lotus japonicus young plan...	2	144	4.30E-07	1
3	G2789	AW216305	AW216305 687047G05.x1 687 - Early embryo fro...	-2	141	4.60E-07	1

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3	G2789	D15459	D15459 RICC0669A Rice callus Oryza sativa cD...	1	142	5.90E-07	1
3	G2789	BG601044	BG601044 EST505939 cSTS Solanum tuberosum cD...	1	141	9.20E-07	1
3	G2789	AW647786	AW647786 EST326240 tomato germinating seedli...	3	137	1.40E-06	1
3	G2789	AL383224	AL383224 MtBC12G03F1 MtBC Medicago truncatul...	2	139	1.40E-06	1
3	G2789	AP003925	AP003925 Oryza sativa chromosome 8 clone OJ1...	-2	130	1.50E-06	2
3	G2789	AP004562	AP004562 Oryza sativa chromosome 8 clone P04...	-1	130	1.80E-06	2
3	G2789	BG582452	BG582452 EST484197 GVN Medicago truncatula c...	3	149	2.20E-06	1
3	G2789	BM299690	BM299690 MCR053G12_23908 Ice plant Lambda Un...	2	145	3.00E-06	1
3	G2789	AI897113	AI897113 EST266556 tomato ovary, TAMU Lycope...	2	134	3.40E-06	1
3	G2789	AW761107	AW761107 sl63c09.y1 Gm-c1027 Glycine max cDN...	1	135	3.70E-06	1
3	G2789	AW223229	AW223229 EST300040 tomato fruit red ripe, TA...	1	140	6.40E-06	1
3	G2789	BG645337	BG645337 EST506956 KV3 Medicago truncatula c...	3	144	1.10E-05	1
3	G2789	BG275315	BG275315 NXSI_142_D09_F NXSI (Nsf Xylem Side...	3	130	1.70E-05	1
3	G2789	AF474373	AF474373 Hordeum vulgare BAC 259I16, complet...	2	147	1.80E-05	1
3	G2789	AW620872	AW620872 sj47g06.y1 Gm-c1033 Glycine max cDN...	3	128	1.80E-05	1
3	G2789	AW164140	AW164140 Ljirnpest20-626-g4 Ljirnp Lambda Hy...	1	126	3.20E-05	1
3	G2789	BE611882	BE611882 sr01b07.y1 Gm-c1049 Glycine max cDN...	1	122	8.40E-05	1
3	G2789	BF639276	BF639276 NF011F11IN1F1092 Insect herbivory M...	2	133	0.00013	1
3	G2789	AI691406	AI691406 606015E08.x1 606 - Ear tissue cDNA ...	-1	132	0.00014	1
3	G2789	BI308494	BI308494 EST529904 GPOD Medicago truncatula ...	2	132	0.00032	1
3	G2789	D43486	D43486 D43486 Rice callus cDNA (H.Uchimiya) ...	3	119	0.00035	1
3	G2789	BH423260	BH423260 BOGGZ42TF BOGG Brassica oleracea ge...	-2	129	0.00038	1
3	G2789	BG418060	BG418060 HVSMEk0021C01f Hordeum vulgare test...	3	131	0.00042	1
3	G2789	BG580062	BG580062 EST481784 GVN Medicago truncatula c...	2	126	0.00055	1
3	G2789	AC108762	AC108762 Oryza sativa chromosome 9 clone OSJ...	-3	134	0.00056	1
3	G2789	BM112694	BM112694 EST560230 potato roots Solanum tube...	1	129	0.00059	1
3	G2789	AW720219	AW720219 LjNEST17b3r Lotus japonicus nodule ...	1	120	0.0024	1
3	G2789	BH707416	BH707416 BOHTM48TR BO_2_3_KB Brassica olerac...	1	124	0.0025	1
3	G2789	AI939164	AI939164 sc67f03.y1 Gm-c1016 Glycine max cDN...	1	107	0.0044	1
3	G2789	AI441147	AI441147 sa59d03.y1 Gm-c1004 Glycine max cDN...	3	107	0.0046	1
3	G2789	AU097090	AU097090 AU097090 Rice shoot Oryza sativa cD...	2	116	0.005	1
3	G2789	AI779587	AI779587 EST260466 tomato susceptible, Corne...	1	117	0.0088	1
3	G2789	BG647551	BG647551 EST509170 HOGA Medicago truncatula ...	2	114	0.014	1

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3	G2789	AW698129	AW698129 NXNV_073_B01_F Nsf Xylem Normal woo...	1	103	0.02	1
3	G2789	BH594393	BH594393 BOGKJ24TR BOGK Brassica oleracea ge...	-2	115	0.023	1
3	G2789	AU181026	AU181026 AU181026 Rice green shoot Oryza sat...	3	101	0.027	1
3	G2789	BM308752	BM308752 sak50a05.y1 Gm-c1036 Glycine max cD...	1	109	0.068	1
3	G2789	AQ912903	AQ912903 nbeb0038P12r CUGI Rice BAC Library ...	2	96	0.07	1
3	G2789	BI642324	BI642324 TZS924 TZS (Sapwood-heartwood trans...	-3	109	0.078	1
3	G2789	BI310579	BI310579 EST5312329 GESD Medicago truncatula...	3	108	0.11	1
3	G2789	BI643921	BI643921 NXPV_129_D06_F NXPV (Nsf Xylem Plan...	1	96	0.12	1
3	G2789	AP004116	AP004116 Oryza sativa chromosome 2 clone OJ1...	1	111	0.19	1
3	G2789	BG593493	BG593493 EST492171 cSTS Solanum tuberosum cD...	1	107	0.19	1
3	G2789	BM136703	BM136703 WHE0476_C06_E12ZS Wheat Fusarium gr...	3	92	0.2	1
3	G2789	BI974612	BI974612 sai70g08.y1 Gm-c1068 Glycine max cD...	3	104	0.27	1
3	G2789	BM093021	BM093021 saj04a05.y1 Gm-c1065 Glycine max cD...	3	102	0.29	1
3	G2789	BE230368	BE230368 99AS716 Rice Seedling Lambda ZAPII ...	1	101	0.29	1
3	G2789	BM341562	BM341562 MEST336-F03.T3 ISUM5-RN Zea mays cD...	-1	103	0.31	1
3	G2789	BE025350	BE025350 945025C05.Y1 945 - Mixed adult tiss...	-1	101	0.44	1
3	G2789	BH698099	BH698099 BOMHI48TR BO_2_3_KB Brassica olerac...	-2	104	0.46	1
3	G2789	BG049445	BG049445 OV1_20_A09.g1_A002 Ovary 1 (OV1) So...	1	101	0.5	1
3	G2789	BE454419	BE454419 HVSMEh0094G09f Hordeum vulgare 5-45...	1	102	0.68	1
3	G2789	BM404166	BM404166 EST578493 potato roots Solanum tube...	3	99	0.68	1
3	G2789	BH549232	BH549232 BOHJI16TF BOHJ Brassica oleracea ge...	3	100	0.78	1
3	G2789	BI430960	BI430960 949063D07.y1 949 - Juvenile leaf an...	2	85	0.84	1
3	G2789	BE601230	BE601230 PI1_90_E07.g1_A002 Pathogen induced...	1	97	0.93	1
3	G2789	AC060755	AC060755 Oryza sativa chromosome 10 BAC OSJN...	-1	100	0.97	1
3	G2789	BG316001	BG316001 sab88d01.y1 Gm-c1032 Glycine max cD...	3	94	0.97	1
3	G2789	AL375620	AL375620 MtBB15H05F1 MtBB Medicago truncatul...	1	93	0.99	1
3	G2789	BH620896	BH620896 1007099E11.x1 1007 - RescueMu Grid ...	3	93	0.997	1
3	G2789	BF274040	BF274040 GA__Eb0019P06f Gossypium arboreum 7...	3	94	0.9992	1
3	G2789	AW225825	AW225825 ST72B11 Pine TriplEx shoot tip libr...	2	90	0.9993	1
3	G2789	BE577148	BE577148 L0-1863T3 Ice plant Lambda Uni-Zap ...	-2	91	0.9998	1
3	G2789	BM526041	BM526041 sal36c08.y1 Gm-c1059 Glycine max cD...	1	91	0.9998	1
3	G2789	BF274574	BF274574 GA__Eb0021G20f Gossypium arboreum 7...	3	92	0.9998	1
3	G2789	GI-15528814	hypothetical protein~similar to Arabidopsi...	1	383	2.70E-35	1

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3	G2789	GI-12643044	AC060755_3 putative AT-Hook DNA-binding pr...	1	272	1.70E-23	1
3	G2789	GI-5042445	AC007789_8 hypothetical protein	1	254	1.60E-20	1
3	G2789	GI-4165183	SAP1 protein	1	233	2.10E-19	1
3	G2789	GI-2213534	DNA-binding PD1-like protein	1	221	4.10E-18	1
3	G2789	GI-7488826	T06582 probable DNA-binding protein - gard...	1	221	4.10E-18	1
3	G2789	GI-2213536	DNA-binding protein PD1	1	221	5.60E-18	1
3	G2789	GI-7488825	T06584 probable DNA-binding protein - gard...	1	221	5.60E-18	1
3	G2789	GI-6069668	hypothetical protein	1	66	0.73	2
3	G2789	GI-5679340	hypothetical protein	-2	59	0.96	1
3	G2789	GI-8096634	ESTs D23743(R0048),AU081353(R0048) corresp...	1	78	0.993	1
3	G2789	GI-5922617	EST C97105(C52004) corresponds to a region...	1	80	0.9997	1
3	G2789	GI-6016850	EST C97105(C52004) corresponds to a region...	1	80	0.9997	1
3	G2789	GI-11034696	hypothetical protein [Oryza sativa]	-2	68	0.99994	1
5	G1945	BG647027	BG647027 EST508646 HOGA Medicago truncatula ...	3	533	1.30E-59	2
5	G1945	BH480897	BH480897 BOGRA01TF BOGR Brassica oleracea ge...	-1	604	1.80E-56	1
5	G1945	BG646893	BG646893 EST508512 HOGA Medicago truncatula ...	2	599	5.00E-56	1
5	G1945	BI426899	BI426899 sag08g12.y1 Gm-c1080 Glycine max cD...	1	525	4.30E-48	1
5	G1945	BF650426	BF650426 NF096G12EC1F1098 Elicited cell cult...	3	507	3.10E-46	1
5	G1945	OSJN00182	AL662981 Oryza sativa chromosome 4 clone OSJ...	1	493	6.00E-44	1
5	G1945	AW574000	AW574000 EST316591 GVN Medicago truncatula c...	1	483	1.00E-43	1
5	G1945	AP004020	AP004020 Oryza sativa chromosome 2 clone OJ1...	2	489	1.60E-43	1
5	G1945	AW774484	AW774484 EST333635 KV3 Medicago truncatula c...	1	480	2.10E-43	1
5	G1945	BG647144	BG647144 EST508763 HOGA Medicago truncatula ...	1	479	2.40E-43	1
5	G1945	BG581882	BG581882 EST483618 GVN Medicago truncatula c...	3	475	6.40E-43	1
5	G1945	BI924382	BI924382 EST544271 tomato flower, buds 0-3 m...	3	473	1.70E-42	1
5	G1945	AP003526	AP003526 Oryza sativa chromosome 6 clone P05...	1	477	3.00E-42	1
5	G1945	AP004165	AP004165 Oryza sativa chromosome 2 clone OJ1...	-3	467	3.40E-41	1
5	G1945	BI308126	BI308126 EST529536 GPOD Medicago truncatula ...	3	459	4.00E-41	1
5	G1945	AW596625	AW596625 sj14f10.y1 Gm-c1032 Glycine max cDN...	2	457	7.50E-41	1
5	G1945	BI971972	BI971972 sag84f09.y1 Gm-c1084 Glycine max cD...	1	457	7.60E-41	1
5	G1945	AP004698	AP004698 Oryza sativa chromosome 8 clone P04...	2	463	9.00E-41	1
5	G1945	BE432188	BE432188 EST398717 tomato breaker fruit, TIG...	3	455	1.30E-40	1
5	G1945	BI699513	BI699513 sag37g08.y1 Gm-c1081 Glycine max cD...	2	452	2.80E-40	1

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5	G1945	AP004635	AP004635 Oryza sativa chromosome 8 clone P06...	-2	458	3.00E-40	1
5	G1945	BH730050	BH730050 BOMEB22TF BO_2_3_KB Brassica olerac...	-1	449	3.40E-40	1
5	G1945	AW278127	AW278127 sf40a09.y1 Gm-c1009 Glycine max cDN...	1	450	4.60E-40	1
5	G1945	BH566718	BH566718 BOHCV23TR BOHC Brassica oleracea ge...	-2	448	4.80E-40	1
5	G1945	BG134451	BG134451 EST467343 tomato crown gall Lycoper...	1	449	5.20E-40	1
5	G1945	AP003891	AP003891 Oryza sativa chromosome 8 clone OJ1...	2	455	6.30E-40	1
5	G1945	AP004587	AP004587 Oryza sativa chromosome 8 clone P05...	3	455	6.30E-40	1
5	G1945	BH660108	BH660108 BOHVI48TF BO_2_3_KB Brassica olerac...	-1	443	1.50E-39	1
5	G1945	AP004757	AP004757 Oryza sativa chromosome 6 clone P06...	-3	448	3.50E-39	1
5	G1945	BH550632	BH550632 BOGUC18TR BOGU Brassica oleracea ge...	-2	435	9.70E-39	1
5	G1945	BM110212	BM110212 EST557748 potato roots Solanum tube...	1	434	1.50E-38	1
5	G1945	BH729110	BH729110 BOHVN82TF BO_2_3_KB Brassica olerac...	-2	433	2.00E-38	1
5	G1945	BH419879	BH419879 BOGGX69TF BOGG Brassica oleracea ge...	-2	426	9.70E-38	1
5	G1945	AL366947	AL366947 MtBA11B10F1 MtBA Medicago truncatul...	1	420	6.70E-37	1
5	G1945	AW980581	AW980581 EST391734 GVN Medicago truncatula c...	3	418	8.70E-37	1
5	G1945	BH685875	BH685875 BOMBO90TR BO_2_3_KB Brassica olerac...	-1	405	2.10E-35	1
5	G1945	BH596283	BH596283 BOGBL42TR BOGB Brassica oleracea ge...	2	401	4.50E-35	1
5	G1945	BH510717	BH510717 BOGGW07TF BOGG Brassica oleracea ge...	1	401	5.30E-35	1
5	G1945	BH481983	BH481983 BOGYI73TR BOGY Brassica oleracea ge...	2	399	7.20E-35	1
5	G1945	BG045781	BG045781 saa06a11.y1 Gm-c1058 Glycine max cD...	3	401	1.00E-34	1
5	G1945	AW776082	AW776082 EST335147 DSIL Medicago truncatula ...	3	398	1.20E-34	1
5	G1945	BF254863	BF254863 HVSMEf0005E05f Hordeum vulgare seed...	2	397	1.50E-34	1
5	G1945	BH717588	BH717588 BOMDB19TF BO_2_3_KB Brassica olerac...	2	396	1.90E-34	1
5	G1945	BH664974	BH664974 BOMBC11TF BO_2_3_KB Brassica olerac...	2	393	3.00E-34	1
5	G1945	BE203784	BE203784 EST396460 KV0 Medicago truncatula c...	2	392	6.80E-34	1
5	G1945	AP003683	AP003683 Oryza sativa genomic DNA, chromosom...	3	396	1.10E-33	1
5	G1945	AV411735	AV411735 AV411735 Lotus japonicus young plan...	1	390	1.20E-33	1
5	G1945	BE999313	BE999313 EST431036 GVSN Medicago truncatula ...	1	309	1.20E-33	2
5	G1945	BF004270	BF004270 EST432768 KV1 Medicago truncatula c...	3	385	3.80E-33	1
5	G1945	BG583687	BG583687 EST485440 GVN Medicago truncatula c...	2	376	2.00E-32	1
5	G1945	AW720668	AW720668 LjNEST14h9rc Lotus japonicus nodule...	1	374	3.90E-32	1
5	G1945	BI321563	BI321563 saf12g07.y3 Gm-c1076 Glycine max cD...	1	372	7.20E-32	1
5	G1945	BH513264	BH513264 BOHQC93TR BOHQ Brassica oleracea ge...	-3	370	8.30E-32	1

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5	G1945	BE805340	BE805340 ss41d08.y1 Gm-c1061 Glycine max cDN...	1	372	1.00E-31	1
5	G1945	BI972076	BI972076 sag85g11.y1 Gm-c1084 Glycine max cD...	2	369	1.50E-31	1
5	G1945	BI419871	BI419871 LjNEST17a9r Lotus japonicus nodule ...	2	368	2.60E-31	1
5	G1945	AW647786	AW647786 EST326240 tomato germinating seedli...	3	362	8.50E-31	1
5	G1945	AP004319	AP004319 Oryza sativa chromosome 1 clone B10...	1	226	8.90E-31	2
5	G1945	BF067277	BF067277 st37f11.y1 Gm-c1067 Glycine max cDN...	3	363	9.20E-31	1
5	G1945	BI701170	BI701170 sag55e11.y1 Gm-c1082 Glycine max cD...	2	359	1.60E-30	1
5	G1945	BG881387	BG881387 sae81e03.y1 Gm-c1065 Glycine max cD...	3	359	1.80E-30	1
5	G1945	BH550963	BH550963 BOHQE85TR BOHQ Brassica oleracea ge...	-3	356	2.50E-30	1
5	G1945	BG583651	BG583651 EST485403 GVN Medicago truncatula c...	3	246	2.50E-30	2
5	G1945	BH459056	BH459056 BOGKX90TR BOGK Brassica oleracea ge...	-2	355	3.30E-30	1
5	G1945	AW761430	AW761430 sl67d09.y1 Gm-c1027 Glycine max cDN...	2	356	4.80E-30	1
5	G1945	BH669958	BH669958 BOMEJ12TF BO_2_3_KB Brassica olerac...	1	349	2.70E-29	1
5	G1945	BM526396	BM526396 sal40g01.y1 Gm-c1059 Glycine max cD...	3	344	7.00E-29	1
5	G1945	BH419964	BH419964 BOGQI28TF BOGQ Brassica oleracea ge...	-1	341	1.70E-28	1
5	G1945	AW350603	AW350603 GM210008B10B12 Gm-r1021 Glycine max...	-1	338	2.20E-28	1
5	G1945	BH688757	BH688757 BOMDL66TF BO_2_3_KB Brassica olerac...	2	338	2.60E-28	1
5	G1945	AI965992	AI965992 sc25a12.y1 Gm-c1013 Glycine max cDN...	3	336	4.60E-28	1
5	G1945	BM779718	BM779718 EST590294 KV2 Medicago truncatula c...	-3	334	5.40E-28	1
5	G1945	AV422634	AV422634 AV422634 Lotus japonicus young plan...	3	335	7.50E-28	1
5	G1945	AW560824	AW560824 EST315872 DSIR Medicago truncatula ...	2	330	2.10E-27	1
5	G1945	AW774872	AW774872 EST334023 KV3 Medicago truncatula c...	3	330	2.90E-27	1
5	G1945	BJ203193	BJ203193 BJ203193 normalized full length cDN...	1	217	3.10E-27	2
5	G1945	AP004680	AP004680 Oryza sativa chromosome 6 clone OSJ...	-1	207	3.70E-27	2
5	G1945	BE998262	BE998262 EST429985 GVSN Medicago truncatula ...	2	326	5.60E-27	1
5	G1945	BM523502	BM523502 sam84f06.y2 Gm-c1087 Glycine max cD...	1	319	2.90E-26	1
5	G1945	AV422959	AV422959 AV422959 Lotus japonicus young plan...	2	320	2.90E-26	1
5	G1945	AW621455	AW621455 EST312253 tomato root during/after ...	2	313	1.00E-25	1
5	G1945	AI960613	AI960613 sc86h10.y1 Gm-c1018 Glycine max cDN...	1	309	4.10E-25	1
5	G1945	AI736668	AI736668 sb32a03.y1 Gm-c1012 Glycine max cDN...	2	307	5.30E-25	1
5	G1945	AV415346	AV415346 AV415346 Lotus japonicus young plan...	3	308	6.00E-25	1
5	G1945	AW648634	AW648634 EST327184 tomato germinating seedli...	3	305	9.10E-25	1
5	G1945	AW349284	AW349284 GM210004B21H7 Gm-r1021 Glycine max ...	-2	301	1.70E-24	1

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5	G1945	BI699401	BI699401 sag36e12.y1 Gm-c1081 Glycine max cD...	1	169	2.40E-24	2
5	G1945	BG132224	BG132224 EST465116 tomato crown gall Lycoper...	2	300	3.50E-24	1
5	G1945	AW780525	AW780525 sl72a07.y1 Gm-c1027 Glycine max cDN...	1	299	6.10E-24	1
5	G1945	BM525692	BM525692 sak62d03.y1 Gm-c1036 Glycine max cD...	1	295	1.00E-23	1
5	G1945	BH430946	BH430946 BOHSM94TF BOHS Brassica oleracea ge...	-1	288	4.70E-23	1
5	G1945	AP003917	AP003917 Oryza sativa chromosome 8 clone OJ1...	3	198	5.00E-23	2
5	G1945	BG599840	BG599840 EST504735 cSTS Solanum tuberosum cD...	3	172	7.10E-23	2
5	G1945	BH679922	BH679922 BOMNO92TR BO_2_3_KB Brassica olerac...	3	281	2.20E-22	1
5	G1945	AW349908	AW349908 GM210006A20F9 Gm-r1021 Glycine max ...	-3	282	2.20E-22	1
5	G1945	BF588135	BF588135 FM1_38_B09.b1_A003 Floral-Induced M...	3	279	5.40E-22	1
5	G1945	BH491363	BH491363 BOGPS71TR BOGP Brassica oleracea ge...	-1	275	9.80E-22	1
5	G1945	BJ189956	BJ189956 BJ189956 normalized full length cDN...	3	271	3.30E-21	1
5	G1945	BI435896	BI435896 EST538657 P. infestans-challenged l...	3	270	7.30E-21	1
5	G1945	BG644865	BG644865 EST506484 KV3 Medicago truncatula c...	2	266	8.70E-21	1
5	G1945	AI494847	AI494847 sb06b09.y1 Gm-c1004 Glycine max cDN...	1	268	9.20E-21	1
5	G1945	AP003938	AP003938 Oryza sativa chromosome 6 clone OJ1...	-2	273	1.20E-20	1
5	G1945	BE020549	BE020549 sm45a11.y1 Gm-c1028 Glycine max cDN...	3	265	2.60E-20	1
5	G1945	BG465540	BG465540 RHIZ2_45_G09.b1_A003 Rhizome2 (RHIZ...	3	263	2.80E-20	1
5	G1945	BE342838	BE342838 EST395682 potato stolon, Cornell Un...	1	260	5.00E-20	1
5	G1945	BE643892	BE643892 NXCI_048_F12_F NXCI (Nsf Xylem Comp...	3	260	7.20E-20	1
5	G1945	AP004303	AP004303 Oryza sativa chromosome 7 clone P04...	2	263	1.40E-19	1
5	G1945	BI972355	BI972355 sag90d06.y1 Gm-c1084 Glycine max cD...	2	254	2.40E-19	1
5	G1945	BI974724	BI974724 sai72b06.y1 Gm-c1068 Glycine max cD...	1	253	2.90E-19	1
5	G1945	BG600318	BG600318 EST505213 cSTS Solanum tuberosum cD...	1	255	3.40E-19	1
5	G1945	BI786439	BI786439 sai49b05.y1 Gm-c1065 Glycine max cD...	1	251	5.10E-19	1
5	G1945	BF187248	BF187248 EST443535 potato stolon, Cornell Un...	2	249	8.50E-19	1
5	G1945	BE445433	BE445433 WHE1136_A09_B18ZS Wheat etiolated s...	2	248	1.00E-18	1
5	G1945	BE442709	BE442709 WHE1105_B09_C17ZS Wheat etiolated s...	3	247	1.30E-18	1
5	G1945	AI522924	AI522924 sa92b03.y1 Gm-c1004 Glycine max cDN...	2	247	1.60E-18	1
5	G1945	BI970749	BI970749 GM830011A20H08 Gm-r1083 Glycine max...	-1	245	1.60E-18	1
5	G1945	AW132605	AW132605 se06d10.y1 Gm-c1013 Glycine max cDN...	3	246	1.70E-18	1
5	G1945	BH173434	BH173434 0104B13 maize genomic ORF library F...	-1	248	1.80E-18	1
5	G1945	AW348874	AW348874 GM210010A10G1 Gm-r1021 Glycine max ...	-2	244	2.00E-18	1

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5	G1945	BE496294	BE496294 NXCI_022_C11_F NXCI (Nsf Xylem Comp...	1	244	3.10E-18	1
5	G1945	BM407572	BM407572 EST581899 potato roots Solanum tube...	1	172	3.70E-18	2
5	G1945	AW672482	AW672482 LG1_360_E08.b1_A002 Light Grown 1 (...	3	242	4.30E-18	1
5	G1945	BE822274	BE822274 GM700017A10A4 Gm-r1070 Glycine max ...	-1	240	5.10E-18	1
5	G1945	AV410107	AV410107 AV410107 Lotus japonicus young plan...	2	242	6.80E-18	1
5	G1945	BE442615	BE442615 WHE1101_G09_M17ZS Wheat etiolated s...	2	239	9.40E-18	1
5	G1945	BG350206	BG350206 084D10 Mature tuber lambda ZAP Sola...	3	236	1.50E-17	1
5	G1945	BI321153	BI321153 saf48b01.y3 Gm-c1077 Glycine max cD...	1	236	1.70E-17	1
5	G1945	BG593477	BG593477 EST492155 cSTS Solanum tuberosum cD...	3	236	1.90E-17	1
5	G1945	BE600816	BE600816 PI1_90_E07.b1_A002 Pathogen induced...	3	232	4.80E-17	1
5	G1945	BI139442	BI139442 F131P74Y Populus flower cDNA librar...	-1	231	6.70E-17	1
5	G1945	BI406306	BI406306 159E11 Mature tuber lambda ZAP Sola...	1	229	1.00E-16	1
5	G1945	BI266587	BI266587 NF099D09IN1F1078 Insect herbivory M...	2	224	3.00E-16	1
5	G1945	BH588550	BH588550 BOHOI48TR BOHO Brassica oleracea ge...	-2	224	3.00E-16	1
5	G1945	BM322182	BM322182 PIC1_1_A05.b1_A002 Pathogen-infecte...	2	223	4.10E-16	1
5	G1945	BM322317	BM322317 PIC1_3_A06.b1_A002 Pathogen-infecte...	2	223	4.10E-16	1
5	G1945	BI946361	BI946361 01104 leafy spurge Lambda HybriZAP ...	1	223	4.10E-16	1
5	G1945	AI522913	AI522913 sa91h08.y1 Gm-c1004 Glycine max cDN...	1	224	4.20E-16	1
5	G1945	BM322320	BM322320 PIC1_3_A09.b1_A002 Pathogen-infecte...	2	223	4.30E-16	1
5	G1945	AW099294	AW099294 sd37h01.y1 Gm-c1016 Glycine max cDN...	2	226	4.40E-16	1
5	G1945	BM322319	BM322319 PIC1_3_A08.b1_A002 Pathogen-infecte...	2	223	4.50E-16	1
5	G1945	BM322185	BM322185 PIC1_1_A08.b1_A002 Pathogen-infecte...	2	223	5.50E-16	1
5	G1945	BM322192	BM322192 PIC1_1_B08.b1_A002 Pathogen-infecte...	2	223	5.50E-16	1
5	G1945	BM322318	BM322318 PIC1_3_A07.b1_A002 Pathogen-infecte...	2	223	5.50E-16	1
5	G1945	BG589060	BG589060 EST490869 MHRP- Medicago truncatula...	1	221	5.60E-16	1
5	G1945	BI929403	BI929403 EST549292 tomato flower, 3 - 8 mm b...	1	219	8.10E-16	1
5	G1945	BF324870	BF324870 su17c07.y1 Gm-c1066 Glycine max cDN...	1	221	8.70E-16	1
5	G1945	BF429428	BF429428 WHE1803_A09_B17ZS Secale cereale an...	1	221	9.40E-16	1
5	G1945	BG441060	BG441060 GA__Ea0011I19f Gossypium arboreum 7...	3	217	1.20E-15	1
5	G1945	AMA132349	AJ132349 Antirrhinum majus mRNA for SAP1 pro...	3	219	1.40E-15	1
5	G1945	AW776953	AW776953 EST336018 DSIL Medicago truncatula ...	2	218	1.40E-15	1
5	G1945	BG241750	BG241750 RHIZ2_50_G05.b1_A003 Rhizome2 (RHIZ...	3	218	1.80E-15	1
5	G1945	AL373204	AL373204 MtBA56C11F1 MtBA Medicago truncatul...	3	217	2.30E-15	1

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5	G1945	BE600623	BE600623 PI1_89_D08.b1_A002 Pathogen induced...	3	216	2.80E-15	1
5	G1945	AW596434	AW596434 sj12d05.y1 Gm-c1032 Glycine max cDN...	2	215	4.60E-15	1
5	G1945	AP003074	AP003074 Oryza sativa genomic DNA, chromosom...	-1	220	5.10E-15	1
5	G1945	AC007789	AC007789 Oryza sativa BAC OSJNBa0049B20 geno...	-1	220	5.10E-15	1
5	G1945	BE609898	BE609898 sq46e12.y1 Gm-c1019 Glycine max cDN...	3	213	5.20E-15	1
5	G1945	AW622329	AW622329 EST313127 tomato root during/after ...	2	213	5.80E-15	1
5	G1945	AV424890	AV424890 AV424890 Lotus japonicus young plan...	3	213	6.60E-15	1
5	G1945	BG651836	BG651836 sad61f05.y1 Gm-c1051 Glycine max cD...	3	212	7.60E-15	1
5	G1945	AW455702	AW455702 707090A08.x1 707 - Mixed adult tiss...	3	211	7.90E-15	1
5	G1945	BG596340	BG596340 EST495018 cSTS Solanum tuberosum cD...	3	210	8.90E-15	1
5	G1945	BM086350	BM086350 sah38h08.y1 Gm-c1036 Glycine max cD...	3	210	1.10E-14	1
5	G1945	BM322184	BM322184 PIC1_1_A07.b1_A002 Pathogen-infecte...	2	211	1.20E-14	1
5	G1945	BF587149	BF587149 FM1_32_G07.b1_A003 Floral-Induced M...	3	210	1.40E-14	1
5	G1945	BM358644	BM358644 GA__Ea0011I19r Gossypium arboreum 7...	3	208	1.50E-14	1
5	G1945	AW761107	AW761107 sl63c09.y1 Gm-c1027 Glycine max cDN...	1	210	1.70E-14	1
5	G1945	AW979681	AW979681 EST341290 tomato root deficiency, C...	1	208	1.70E-14	1
5	G1945	AW066510	AW066510 660015F03.y1 660 - Mixed stages of ...	1	206	3.20E-14	1
5	G1945	BG909764	BG909764 TaLr1108d02R TaLr1 Triticum aestivu...	3	205	3.90E-14	1
5	G1945	BE555817	BE555817 sp94c01.y1 Gm-c1045 Glycine max cDN...	3	204	4.90E-14	1
5	G1945	AW928863	AW928863 EST337651 tomato flower buds 8 mm t...	3	203	6.00E-14	1
5	G1945	BM173594	BM173594 900948 Avicennia marina leaf cDNA L...	2	206	6.60E-14	1
5	G1945	BI788210	BI788210 sag68a10.y1 Gm-c1082 Glycine max cD...	3	202	7.30E-14	1
5	G1945	BE330349	BE330349 so77e09.y1 Gm-c1040 Glycine max cDN...	3	201	1.00E-13	1
5	G1945	AW448258	AW448258 BRY_1522 BRY Triticum aestivum cDNA...	3	199	1.10E-13	1
5	G1945	BE586257	BE586257 WHE501_B07_C13ZR Secale cereale alu...	2	200	1.20E-13	1
5	G1945	BG599554	BG599554 EST504449 cSTS Solanum tuberosum cD...	2	198	1.50E-13	1
5	G1945	BE496149	BE496149 WHE1262_H03_P06ZS Secale cereale an...	2	200	1.50E-13	1
5	G1945	BG240061	BG240061 OV1_17_D10.b1_A002 Ovary 1 (OV1) So...	1	199	1.60E-13	1
5	G1945	BH732637	BH732637 BOMBI03TF BO_2_3_KB Brassica olerac...	2	198	1.60E-13	1
5	G1945	BG240043	BG240043 OV1_17_B12.b1_A002 Ovary 1 (OV1) So...	1	199	1.60E-13	1
5	G1945	D42950	D42950 D42950 Rice callus cDNA (H.Uchimiya) ...	2	200	1.70E-13	1
5	G1945	BM094108	BM094108 sah25e08.y1 Gm-c1036 Glycine max cD...	1	198	2.20E-13	1
5	G1945	AW755831	AW755831 sl09h02.y1 Gm-c1036 Glycine max cDN...	3	198	2.70E-13	1

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5	G1945	BG583795	BG583795 EST485550 GVN Medicago truncatula c...	1	195	3.10E-13	1
5	G1945	AL508367	AL508367 AL508367 Hordeum vulgare Barke deve...	3	195	3.60E-13	1
5	G1945	AV917319	AV917319 AV917319 K. Sato unpublished cDNA l...	2	195	3.60E-13	1
5	G1945	BM371214	BM371214 EBro04_SQ003_M20_R IGF Barley EBro0...	2	196	4.70E-13	1
5	G1945	AW906401	AW906401 EST342523 potato stolon, Cornell Un...	2	195	4.70E-13	1
5	G1945	BF637181	BF637181 NF050F02LF1F1016 Developing leaf Me...	3	194	5.00E-13	1
5	G1945	BM094106	BM094106 sah25e06.y1 Gm-c1036 Glycine max cD...	1	194	5.80E-13	1
5	G1945	BI074657	BI074657 IP1_14_F04.b1_A002 Immature pannicl...	1	193	6.40E-13	1
5	G1945	BE591277	BE591277 WHE1655-1658_J17_J17ZS Wheat heat s...	1	192	8.40E-13	1
5	G1945	AW755604	AW755604 sl05h07.y1 Gm-c1036 Glycine max cDN...	3	191	1.00E-12	1
5	G1945	BE444180	BE444180 WHE1128_B06_D12ZS Wheat etiolated s...	2	190	1.60E-12	1
5	G1945	AL372048	AL372048 MtBA48C06F1 MtBA Medicago truncatul...	1	191	1.70E-12	1
5	G1945	BH650598	BH650598 BOHZR58TR BO_2_3_KB Brassica olerac...	1	185	4.30E-12	1
5	G1945	BG240220	BG240220 OV1_19_D02.b1_A002 Ovary 1 (OV1) So...	1	185	6.20E-12	1
5	G1945	BE587763	BE587763 WHE0652_C06_E12ZM Secale cereale ro...	1	184	6.70E-12	1
5	G1945	AI881841	AI881841 606074A03.y1 606 - Ear tissue cDNA ...	3	182	9.10E-12	1
5	G1945	BH596271	BH596271 BOGBL42TF BOGB Brassica oleracea ge...	-3	184	1.10E-11	1
5	G1945	BE807468	BE807468 ss22h03.y1 Gm-c1047 Glycine max cDN...	2	182	1.40E-11	1
5	G1945	BF636643	BF636643 NF091G07DT1F1055 Drought Medicago t...	1	181	1.40E-11	1
5	G1945	PSDBLPPD1	X98739 P.sativum mRNA encoding DNA-binding P...	1	194	1.80E-11	1
5	G1945	BG352828	BG352828 sab91g04.y1 Gm-c1040 Glycine max cD...	3	180	1.80E-11	1
5	G1945	BM136003	BM136003 WHE2604_D04_H08ZS Wheat Fusarium gr...	-1	179	1.90E-11	1
5	G1945	PSDBPPD1	X98738 P.sativum mRNA encoding DNA-binding p...	1	194	2.30E-11	1
5	G1945	AI988292	AI988292 sc98f12.y1 Gm-c1020 Glycine max cDN...	2	178	2.60E-11	1
5	G1945	BG043009	BG043009 st91a08.y1 Gm-c1054 Glycine max cDN...	3	180	2.60E-11	1
5	G1945	AI443215	AI443215 sa45h07.y1 Gm-c1004 Glycine max cDN...	1	178	3.90E-11	1
5	G1945	AW310124	AW310124 sf31d10.x1 Gm-c1028 Glycine max cDN...	-1	176	4.30E-11	1
5	G1945	BG130143	BG130143 EST475789 tomato shoot/meristem Lyc...	1	175	5.20E-11	1
5	G1945	BE345655	BE345655 946021H10.y2 946 - tassel primordiu...	3	175	6.40E-11	1
5	G1945	BJ186205	BJ186205 BJ186205 normalized full length cDN...	1	174	8.20E-11	1
5	G1945	BF625927	BF625927 HVSMEa0014H11f Hordeum vulgare seed...	1	173	1.30E-10	1
5	G1945	BI931107	BI931107 EST550996 tomato flower, 8 mm to pr...	1	171	1.70E-10	1
5	G1945	BI096714	BI096714 949019H11.y1 949 - Juvenile leaf an...	2	171	2.00E-10	1

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5	G1945	BI932139	BI932139 EST552028 tomato flower, 8 mm to pr...	1	178	2.20E-10	1
5	G1945	BE202989	BE202989 EST403011 KV1 Medicago truncatula c...	-3	170	2.60E-10	1
5	G1945	BI469296	BI469296 sai10a11.y1 Gm-c1053 Glycine max cD...	3	170	3.10E-10	1
5	G1945	BF258208	BF258208 HVSMEf0015B16f Hordeum vulgare seed...	2	177	3.30E-10	1
5	G1945	BG888793	BG888793 EST514644 cSTD Solanum tuberosum cD...	3	178	3.30E-10	1
5	G1945	BM307331	BM307331 sak27h05.y1 Gm-c1075 Glycine max cD...	1	169	3.50E-10	1
5	G1945	BM521838	BM521838 sak76f11.y1 Gm-c1036 Glycine max cD...	2	167	5.60E-10	1
5	G1945	BI700385	BI700385 sag60b11.y1 Gm-c1082 Glycine max cD...	2	167	7.40E-10	1
5	G1945	BI267267	BI267267 NF100C06IN1F1070 Insect herbivory M...	2	122	8.90E-10	2
5	G1945	BF112609	BF112609 EST440199 tomato breaker fruit Lyco...	3	162	2.50E-09	1
5	G1945	BI434654	BI434654 EST537415 P. infestans-challenged I...	1	165	2.50E-09	1
5	G1945	AI897688	AI897688 EST267131 tomato ovary, TAMU Lycope...	3	161	3.10E-09	1
5	G1945	BI928278	BI928278 EST548167 tomato flower, 3 - 8 mm b...	1	171	3.20E-09	1
5	G1945	BI929489	BI929489 EST549378 tomato flower, 3 - 8 mm b...	1	171	4.20E-09	1
5	G1945	BI927526	BI927526 EST547415 tomato flower, 3 - 8 mm b...	3	165	4.80E-09	1
5	G1945	BE923864	BE923864 EST427633 potato leaves and petiole...	1	160	4.80E-09	1
5	G1945	BM524672	BM524672 sal18d07.y1 Gm-c1059 Glycine max cD...	2	159	4.90E-09	1
5	G1945	BM524654	BM524654 sal18b12.y1 Gm-c1059 Glycine max cD...	2	159	5.10E-09	1
5	G1945	BI430562	BI430562 949057A04.y1 949 - Juvenile leaf an...	1	157	7.80E-09	1
5	G1945	BM405827	BM405827 EST580154 potato roots Solanum tube...	2	158	8.60E-09	1
5	G1945	AV423934	AV423934 AV423934 Lotus japonicus young plan...	3	158	8.80E-09	1
5	G1945	BM079070	BM079070 MEST88-H11.T3 ISUM4-TN Zea mays cDN...	-1	166	9.10E-09	1
5	G1945	AW773742	AW773742 EST332728 KV3 Medicago truncatula c...	3	156	1.00E-08	1
5	G1945	AU198263	AU198263 AU198263 Rice green shoot Oryza sat...	1	157	1.00E-08	1
5	G1945	BJ158045	BJ158045 BJ158045 full length cDNA library, ...	-3	156	1.10E-08	1
5	G1945	BM412174	BM412174 EST586501 tomato breaker fruit Lyco...	1	159	1.20E-08	1
5	G1945	BG601044	BG601044 EST505939 cSTS Solanum tuberosum cD...	1	155	1.30E-08	1
5	G1945	AW760534	AW760534 sl51e09.y1 Gm-c1027 Glycine max cDN...	1	153	2.30E-08	1
5	G1945	AW720136	AW720136 LjNEST14h9r Lotus japonicus nodule ...	1	154	2.60E-08	1
5	G1945	BG594217	BG594217 EST492895 cSTS Solanum tuberosum cD...	2	152	2.80E-08	1
5	G1945	BE357932	BE357932 DG1_23_D12.b1_A002 Dark Grown 1 (DG...	1	152	3.00E-08	1
5	G1945	AW773741	AW773741 EST332727 KV3 Medicago truncatula c...	3	152	3.00E-08	1
5	G1945	BE923621	BE923621 EST427390 potato leaves and petiole...	1	152	3.70E-08	1

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5	G1945	BE125776	BE125776 DG1_57_B07.b1_A002 Dark Grown 1 (DG...	1	152	4.20E-08	1
5	G1945	AW309814	AW309814 sf25b03.x1 Gm-c1028 Glycine max cDN...	-1	156	1.20E-07	1
5	G1945	BG239709	BG239709 sab74e11.y1 Gm-c1032 Glycine max cD...	3	146	1.40E-07	1
5	G1945	AV411140	AV411140 AV411140 Lotus japonicus young plan...	2	147	1.50E-07	1
5	G1945	AV425818	AV425818 AV425818 Lotus japonicus young plan...	3	147	1.60E-07	1
5	G1945	BH439306	BH439306 BOHGL38TR BOHG Brassica oleracea ge...	1	146	1.60E-07	1
5	G1945	BG098673	BG098673 EST463192 sprouting eyes/shoots Sol...	2	148	1.80E-07	1
5	G1945	BF257835	BF257835 HVSMEf0014A01f Hordeum vulgare seed...	2	144	2.50E-07	1
5	G1945	BJ196157	BJ196157 BJ196157 normalized full length cDN...	1	146	2.90E-07	1
5	G1945	AW394835	AW394835 sh36a01.y1 Gm-c1017 Glycine max cDN...	2	143	3.40E-07	1
5	G1945	BM427899	BM427899 NXRV_006_A04_F NXRV (Nsf Xylem Root...	1	143	3.80E-07	1
5	G1945	AW620872	AW620872 sj47g06.y1 Gm-c1033 Glycine max cDN...	3	143	4.30E-07	1
5	G1945	AW776126	AW776126 EST335191 DSIL Medicago truncatula ...	2	154	5.30E-07	1
5	G1945	AW720219	AW720219 LjNEST17b3r Lotus japonicus nodule ...	-1	141	5.50E-07	1
5	G1945	AV421337	AV421337 AV421337 Lotus japonicus young plan...	2	143	6.50E-07	1
5	G1945	BM441160	BM441160 EBed02_SQ002_J15_R IGF Barley EBed0...	1	138	1.20E-06	1
5	G1945	BG643949	BG643949 EST512143 tomato shoot/meristem Lyc...	2	151	1.30E-06	1
5	G1945	BG582457	BG582457 EST484202 GVN Medicago truncatula c...	3	138	1.80E-06	1
5	G1945	AI779587	AI779587 EST260466 tomato susceptible, Corne...	1	142	2.00E-06	1
5	G1945	D15459	D15459 RICC0669A Rice callus Oryza sativa cD...	1	136	3.20E-06	1
5	G1945	AI487942	AI487942 EST246264 tomato ovary, TAMU Lycope...	1	137	3.30E-06	1
5	G1945	AI507693	AI507693 sb10d09.y1 Gm-c1004 Glycine max cDN...	2	134	3.50E-06	1
5	G1945	AP004116	AP004116 Oryza sativa chromosome 2 clone OJ1...	1	153	4.40E-06	1
5	G1945	AW031261	AW031261 EST274636 tomato callus, TAMU Lycop...	1	143	4.90E-06	1
5	G1945	BG604965	BG604965 WHE2325_E05_I09ZS Wheat pre-anthesi...	3	132	6.90E-06	1
5	G1945	AV412906	AV412906 AV412906 Lotus japonicus young plan...	3	132	1.10E-05	1
5	G1945	AW164140	AW164140 Ljirnpest20-626-g4 Ljirnp Lambda Hy...	1	128	2.10E-05	1
5	G1945	D43486	D43486 D43486 Rice callus cDNA (H.Uchimiya) ...	3	129	3.00E-05	1
5	G1945	BG592977	BG592977 EST491655 cSTS Solanum tuberosum cD...	-2	136	3.20E-05	1
5	G1945	BG149109	BG149109 48 LIN01 Lupinus luteus cDNA, mRNA ...	3	125	4.40E-05	1
5	G1945	BG040551	BG040551 NXSI_112_D08_F NXSI (Nsf Xylem Side...	1	125	4.50E-05	1
5	G1945	BG510489	BG510489 sac78f02.y1 Gm-c1072 Glycine max cD...	3	129	5.30E-05	1
5	G1945	BF639276	BF639276 NF011F11IN1F1092 Insect herbivory M...	2	135	8.40E-05	1

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5	G1945	BI675167	BI675167 949079C12.x2 949 - Juvenile leaf an...	-2	132	0.0001	1
5	G1945	BG275315	BG275315 NXSI_142_D09_F NXSI (Nsf Xylem Side...	3	120	0.00024	1
5	G1945	BE446692	BE446692 WHE1139_D09_H17ZS Wheat etiolated s...	2	118	0.00027	1
5	G1945	BG645337	BG645337 EST506956 KV3 Medicago truncatula c...	3	132	0.00037	1
5	G1945	AI691406	AI691406 606015E08.x1 606 - Ear tissue cDNA ...	-1	129	0.00038	1
5	G1945	BG582452	BG582452 EST484197 GVN Medicago truncatula c...	3	131	0.00041	1
5	G1945	AW216305	AW216305 687047G05.x1 687 - Early embryo fro...	-2	125	0.00076	1
5	G1945	BM299690	BM299690 MCR053G12_23908 Ice plant Lambda Un...	2	127	0.00079	1
5	G1945	AI460865	AI460865 sa70c03.y1 Gm-c1004 Glycine max cDN...	3	109	0.0026	1
5	G1945	AU097090	AU097090 AU097090 Rice shoot Oryza sativa cD...	2	118	0.0029	1
5	G1945	BM093021	BM093021 saj04a05.y1 Gm-c1065 Glycine max cD...	3	116	0.0031	1
5	G1945	AL383224	AL383224 MtBC12G03F1 MtBC Medicago truncatul...	2	109	0.0036	1
5	G1945	AW929149	AW929149 EST337937 tomato flower buds 8 mm t...	2	121	0.0045	1
5	G1945	BM404166	BM404166 EST578493 potato roots Solanum tube...	3	118	0.0047	1
5	G1945	BM309583	BM309583 sak64c09.y1 Gm-c1036 Glycine max cD...	1	117	0.0085	1
5	G1945	BI643921	BI643921 NXPV_129_D06_F NXPV (Nsf Xylem Plan...	1	107	0.0087	1
5	G1945	BG323043	BG323043 EM1_14_C04.g1_A002 Embryo 1 (EM1) S...	2	112	0.021	1
5	G1945	AP003925	AP003925 Oryza sativa chromosome 8 clone OJ1...	-2	120	0.023	1
5	G1945	AP004562	AP004562 Oryza sativa chromosome 8 clone P04...	-1	120	0.023	1
5	G1945	BI934755	BI934755 EST554644 tomato flower, anthesis L...	2	114	0.035	1
5	G1945	AI441147	AI441147 sa59d03.y1 Gm-c1004 Glycine max cDN...	3	99	0.037	1
5	G1945	BH707416	BH707416 BOHTM48TR BO_2_3_KB Brassica olerac...	1	114	0.041	1
5	G1945	BI308494	BI308494 EST529904 GPOD Medicago truncatula ...	2	114	0.045	1
5	G1945	AL375620	AL375620 MtBB15H05F1 MtBB Medicago truncatul...	1	108	0.047	1
5	G1945	BF587998	BF587998 FM1_35_D12.g1_A003 Floral-Induced M...	2	110	0.053	1
5	G1945	BG051900	BG051900 RHIZ2_6_C11.g1_A003 Rhizome2 (RHIZ2...	1	110	0.065	1
5	G1945	BM112694	BM112694 EST560230 potato roots Solanum tube...	1	112	0.065	1
5	G1945	BI974612	BI974612 sai70g08.y1 Gm-c1068 Glycine max cD...	3	109	0.077	1
5	G1945	BI788421	BI788421 sag70e10.y1 Gm-c1082 Glycine max cD...	3	105	0.078	1
5	G1945	AU181026	AU181026 AU181026 Rice green shoot Oryza sat...	3	96	0.099	1
5	G1945	AY023527	AY023527 Oryza sativa microsatellite MRG5852...	2	97	0.1	1
5	G1945	BE399704	BE399704 WHE0041.G04F990703 ITEC WHE Wheat E...	-1	95	0.11	1
5	G1945	BI132051	BI132051 G130P25Y Populus cambium cDNA libra...	-3	94	0.13	1

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5	G1945	BE025350	BE025350 945025C05.Y1 945 - Mixed adult tiss...	-1	106	0.14	1
5	G1945	AI494950	AI494950 sa93a09.y1 Gm-c1004 Glycine max cDN...	1	96	0.15	1
5	G1945	BM341562	BM341562 MEST336-F03.T3 ISUM5-RN Zea mays cD...	-1	106	0.16	1
5	G1945	BI310579	BI310579 EST5312329 GESD Medicago truncatula...	3	107	0.16	1
5	G1945	AI778305	AI778305 EST259184 tomato susceptible, Corne...	-1	93	0.18	1
5	G1945	AW679238	AW679238 WS1_23_B12.b1_A002 Water-stressed 1...	-2	93	0.18	1
5	G1945	BI643533	BI643533 949079C12.x1 949 - Juvenile leaf an...	-3	106	0.18	1
5	G1945	AV639347	AV639347 AV639347 Chlamydomonas reinhardtii ...	-3	95	0.18	1
5	G1945	AY022612	AY022612 Oryza sativa microsatellite MRG4937...	-3	94	0.2	1
5	G1945	AY022633	AY022633 Oryza sativa microsatellite MRG4958...	-3	94	0.21	1
5	G1945	BG133546	BG133546 EST466534 tomato crown gall Lycoper...	-1	93	0.21	1
5	G1945	AF333786	AF333786 Pinus taeda microsatellite PtTX3112...	-2	92	0.21	1
5	G1945	AV408212	AV408212 AV408212 Lotus japonicus young plan...	-2	92	0.21	1
5	G1945	BE604986	BE604986 WHE1713-1716_G09_G09ZS Wheat heat s...	-3	92	0.22	1
5	G1945	BG558570	BG558570 RHIZ2_57_E07.g1_A003 Rhizome2 (RHIZ...	-2	93	0.22	1
5	G1945	AB053190	AB053190 Salix reinii DNA, microsatellite ma...	3	93	0.22	1
5	G1945	AW037795	AW037795 EST279424 tomato mixed elicitor, BT...	-3	93	0.23	1
5	G1945	BE422691	BE422691 WHE0058_H09_P18ZS Wheat endosperm c...	-1	92	0.23	1
5	G1945	BG649667	BG649667 RHIZ2_82_C04.b1_A003 Rhizome2 (RHIZ...	1	104	0.23	1
5	G1945	AY022614	AY022614 Oryza sativa microsatellite MRG4939...	-3	93	0.24	1
5	G1945	BE424188	BE424188 WHE0075_F08_K15ZS Wheat endosperm c...	-1	92	0.25	1
5	G1945	BG313013	BG313013 WHE0091_B12_C23ZS Wheat endosperm c...	-1	91	0.26	1
5	G1945	BE428463	BE428463 MTD007.C10F990616 ITEC MTD Durum Wh...	2	91	0.26	1
5	G1945	BG130209	BG130209 EST475855 tomato shoot/meristem Lyc...	-2	91	0.27	1
5	G1945	BE424140	BE424140 WHE0076_D05_G10ZS Wheat endosperm c...	-2	92	0.27	1
5	G1945	BM112790	BM112790 EST560326 potato roots Solanum tube...	3	104	0.27	1
5	G1945	BE399709	BE399709 WHE0041.G09F990703 ITEC WHE Wheat E...	-3	91	0.27	1
5	G1945	AI165282	AI165282 A080P32U Hybrid aspen plasmid libra...	-3	91	0.27	1
5	G1945	AW776153	AW776153 EST335218 DSIL Medicago truncatula ...	-1	91	0.27	1
5	G1945	BM308752	BM308752 sak50a05.y1 Gm-c1036 Glycine max cD...	1	104	0.28	1
5	G1945	AY022616	AY022616 Oryza sativa microsatellite MRG4941...	-3	92	0.28	1
5	G1945	AY023677	AY023677 Oryza sativa microsatellite MRG6002...	3	92	0.28	1
5	G1945	BE398936	BE398936 WHE0028.B04F990514 ITEC WHE Wheat E...	-1	92	0.28	1

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5	G1945	AY022615	AY022615 Oryza sativa microsatellite MRG4940...	-3	92	0.28	1
5	G1945	AY023559	AY023559 Oryza sativa microsatellite MRG5884...	2	92	0.28	1
5	G1945	AW568964	AW568964 si73f11.y1 Gm-c1031 Glycine max cDN...	-2	91	0.3	1
5	G1945	AU093677	AU093677 AU093677 Rice callus Oryza sativa c...	-1	91	0.31	1
5	G1945	BF293447	BF293447 WHE2152_E10_I20ZS Triticum turgidum...	-3	90	0.32	1
5	G1945	BI325443	BI325443 949038H11.y2 949 - Juvenile leaf an...	-3	90	0.32	1
5	G1945	BM521214	BM521214 sal12a04.y1 Gm-c1057 Glycine max cD...	-1	90	0.32	1
5	G1945	BG263078	BG263078 WHE0946_G12_M24ZS Wheat 5-15 DAP sp...	-3	92	0.32	1
5	G1945	BH599467	BH599467 BOGNL80TF BOGN Brassica oleracea ge...	3	106	0.32	1
5	G1945	BF293865	BF293865 WHE2153_H09_P17ZS Triticum turgidum...	-1	90	0.32	1
5	G1945	BF294028	BF294028 WHE2161_C01_F01ZS Triticum turgidum...	-3	90	0.32	1
5	G1945	LSA17623	Y17623 Lactuca sativa SSR microsatellite seq...	-1	90	0.32	1
5	G1945	LSA17629	Y17629 Lactuca sativa SSR microsatellite seq...	-1	90	0.32	1
5	G1945	BE399219	BE399219 WHE0032.C01F990514 ITEC WHE Wheat E...	-2	90	0.32	1
5	G1945	BE399375	BE399375 WHE0035.D07F990516 ITEC WHE Wheat E...	3	90	0.33	1
5	G1945	AV627762	AV627762 AV627762 Chlamydomonas reinhardtii ...	-3	90	0.33	1
5	G1945	BE438437	BE438437 WHE0019.C06R000701 ITEC WHE Wheat E...	-2	95	0.33	1
5	G1945	AW395964	AW395964 sh01e05.y1 Gm-c1026 Glycine max cDN...	-2	90	0.33	1
5	G1945	AW266214	AW266214 L30-2919T3 Ice plant Lambda Uni-Zap...	1	90	0.33	1
5	G1945	AV641772	AV641772 AV641772 Chlamydomonas reinhardtii ...	-3	90	0.33	1
5	G1945	AW348093	AW348093 GM210001A11E8 Gm-r1021 Glycine max ...	1	90	0.33	1
5	G1945	AV413481	AV413481 AV413481 Lotus japonicus young plan...	-3	90	0.34	1
5	G1945	AY022617	AY022617 Oryza sativa microsatellite MRG4942...	-3	90	0.34	1
5	G1945	LSA17618	Y17618 Lactuca sativa SSR microsatellite seq...	-3	90	0.34	1
5	G1945	BE428321	BE428321 MTD005.G01F990616 ITEC MTD Durum Wh...	2	90	0.34	1
5	G1945	AF072898	AF072898 Triticum monococcum low molecular w...	-2	90	0.34	1
5	G1945	AW034730	AW034730 EST278532 tomato callus, TAMU Lycop...	-3	90	0.34	1
5	G1945	AV417568	AV417568 AV417568 Lotus japonicus young plan...	-3	90	0.35	1
5	G1945	BE399956	BE399956 WHE0044.A11F990602 ITEC WHE Wheat E...	-3	90	0.35	1
5	G1945	LSA17621	Y17621 Lactuca sativa SSR microsatellite seq...	-3	90	0.35	1
5	G1945	BM373703	BM373703 EBma03_SQ002_G10_R IGF Barley EBma0...	-2	90	0.36	1
5	G1945	BE601230	BE601230 PI1_90_E07.g1_A002 Pathogen induced...	1	104	0.36	1
5	G1945	AW307162	AW307162 sf53e10.y1 Gm-c1009 Glycine max cDN...	-1	90	0.36	1

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5	G1945	BG263486	BG263486 WHE2342_E10_I20ZS Wheat pre-anthesi...	-1	90	0.36	1
5	G1945	LSA17625	Y17625 Lactuca sativa SSR microsatellite seq...	-2	90	0.36	1
5	G1945	AW060104	AW060104 687002C04.x1 687 - Early embryo fro...	3	90	0.36	1
5	G1945	AI166086	AI166086 B007P72U Hybrid aspen plasmid libra...	-1	90	0.36	1
5	G1945	AV626412	AV626412 AV626412 Chlamydomonas reinhardtii ...	-2	99	0.36	1
5	G1945	BE398816	BE398816 WHE0026.D01F990702 ITEC WHE Wheat E...	-2	90	0.36	1
5	G1945	AV642035	AV642035 AV642035 Chlamydomonas reinhardtii ...	-2	90	0.36	1
5	G1945	AY023334	AY023334 Oryza sativa microsatellite MRG5659...	1	91	0.37	1
5	G1945	AF172409	AF172409 Pinus taeda clone LC10o2 microsatel...	1	90	0.37	1
5	G1945	BE438282	BE438282 WHE0007.A07R000701 ITEC WHE Wheat E...	-2	90	0.37	1
5	G1945	AY023333	AY023333 Oryza sativa microsatellite MRG5658...	1	91	0.37	1
5	G1945	BI203163	BI203163 AC22R Almond Lambda Zap II cDNA Lib...	-2	90	0.37	1
5	G1945	BE399590	BE399590 WHE0038.D08F990516 ITEC WHE Wheat E...	-2	90	0.37	1
5	G1945	BE473568	BE473568 sp52f10.y1 Gm-c1043 Glycine max cDN...	1	90	0.37	1
5	G1945	BE398786	BE398786 WHE0025.G02F990702 ITEC WHE Wheat E...	-2	90	0.37	1
5	G1945	AF143970	AF143970 Pinus taeda microsatellite PtTX3025...	-2	90	0.37	1
5	G1945	BG263024	BG263024 WHE0946_B09_C18ZS Wheat 5-15 DAP sp...	-3	91	0.37	1
5	G1945	AY022967	AY022967 Oryza sativa microsatellite MRG5292...	3	91	0.37	1
5	G1945	BE428189	BE428189 MTD004.C07F990616 ITEC MTD Durum Wh...	2	90	0.38	1
5	G1945	LSA17615	Y17615 Lactuca sativa SSR microsatellite seq...	-3	90	0.38	1
5	G1945	AY022273	AY022273 Oryza sativa microsatellite MRG4598...	-1	91	0.38	1
5	G1945	AY023670	AY023670 Oryza sativa microsatellite MRG5995...	3	91	0.38	1
5	G1945	BE399860	BE399860 WHE0041.B04F990703 ITEC WHE Wheat E...	-3	90	0.38	1
5	G1945	AY022534	AY022534 Oryza sativa microsatellite MRG4859...	1	90	0.38	1
5	G1945	BG316001	BG316001 sab88d01.y1 Gm-c1032 Glycine max cD...	3	101	0.38	1
5	G1945	LSA17622	Y17622 Lactuca sativa SSR microsatellite seq...	-1	90	0.38	1
5	G1945	BI928792	BI928792 EST548681 tomato flower, 3 - 8 mm b...	-1	90	0.38	1
5	G1945	BF293320	BF293320 WHE2155_B12_C23ZS Triticum turgidum...	-2	92	0.39	1
5	G1945	BE604742	BE604742 WHE1713-1716_I04_I04ZS Wheat heat s...	-1	90	0.39	1
5	G1945	AY023479	AY023479 Oryza sativa microsatellite MRG5804...	2	91	0.39	1
5	G1945	LSA17631	Y17631 Lactuca sativa SSR microsatellite seq...	-3	90	0.39	1
5	G1945	BJ163808	BJ163808 BJ163808 full length cDNA library, ...	1	90	0.39	1
5	G1945	BF294040	BF294040 WHE2161_D10_H19ZS Triticum turgidum...	-2	92	0.4	1

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5	G1945	AY022413	AY022413 Oryza sativa microsatellite MRG4738...	-2	90	0.4	1
5	G1945	AI163924	AI163924 A051P41U Hybrid aspen plasmid libra...	-2	94	0.4	1
5	G1945	AY022275	AY022275 Oryza sativa microsatellite MRG4600...	-1	90	0.41	1
5	G1945	BF428793	BF428793 WHE1711_E08_J15ZS Wheat heat stress...	-3	90	0.41	1
5	G1945	AW234929	AW234929 sf20g11.y1 Gm-c1028 Glycine max cDN...	3	90	0.41	1
5	G1945	BF293713	BF293713 WHE2154_B05_D10ZS Triticum turgidum...	-1	90	0.41	1
5	G1945	AY023357	AY023357 Oryza sativa microsatellite MRG5682...	-3	90	0.42	1
5	G1945	BE590468	BE590468 WHE0854_F11_L22ZS Wheat 20-45 DAP s...	-2	90	0.43	1
5	G1945	AY023676	AY023676 Oryza sativa microsatellite MRG6001...	3	90	0.43	1
5	G1945	BF293469	BF293469 WHE2152_G11_M22ZS Triticum turgidum...	-3	90	0.43	1
5	G1945	AY022412	AY022412 Oryza sativa microsatellite MRG4737...	-2	90	0.43	1
5	G1945	BI317506	BI317506 saf66h01.y1 Gm-c1078 Glycine max cD...	-2	90	0.43	1
5	G1945	AF143968	AF143968 Pinus taeda microsatellite PtTX3019...	-1	90	0.43	1
5	G1945	AY022410	AY022410 Oryza sativa microsatellite MRG4735...	-2	90	0.44	1
5	G1945	AY022411	AY022411 Oryza sativa microsatellite MRG4736...	-2	90	0.44	1
5	G1945	AY023335	AY023335 Oryza sativa microsatellite MRG5660...	1	90	0.44	1
5	G1945	AY023675	AY023675 Oryza sativa microsatellite MRG6000...	3	90	0.44	1
5	G1945	AY023674	AY023674 Oryza sativa microsatellite MRG5999...	3	90	0.44	1
5	G1945	LSA17628	Y17628 Lactuca sativa SSR microsatellite seq...	-3	90	0.44	1
5	G1945	AI442433	AI442433 sa26h01.y1 Gm-c1004 Glycine max cDN...	-2	90	0.44	1
5	G1945	AF354407	AF354407 Corymbia variegata clone EMCRC27 mi...	3	90	0.44	1
5	G1945	AI745835	AI745835 605074A05.x1 605 - Endosperm cDNA l...	3	90	0.44	1
5	G1945	AW284547	AW284547 LG1_270_E03.g1_A002 Light Grown 1 (...	3	98	0.45	1
5	G1945	AY023332	AY023332 Oryza sativa microsatellite MRG5657...	1	90	0.45	1
5	G1945	BJ203431	BJ203431 BJ203431 normalized full length cDN...	1	92	0.45	1
5	G1945	AY023558	AY023558 Oryza sativa microsatellite MRG5883...	2	90	0.45	1
5	G1945	AY023672	AY023672 Oryza sativa microsatellite MRG5997...	3	90	0.45	1
5	G1945	AY023673	AY023673 Oryza sativa microsatellite MRG5998...	3	90	0.45	1
5	G1945	AF143966	AF143966 Pinus taeda microsatellite PtTX3013...	2	90	0.45	1
5	G1945	AY022640	AY022640 Oryza sativa microsatellite MRG4965...	-3	90	0.46	1
5	G1945	AY023540	AY023540 Oryza sativa microsatellite MRG5865...	2	90	0.46	1
5	G1945	AY022274	AY022274 Oryza sativa microsatellite MRG4599...	-1	90	0.46	1
5	G1945	AY022613	AY022613 Oryza sativa microsatellite MRG4938...	-3	90	0.46	1

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5	G1945	AY022641	AY022641 Oryza sativa microsatellite MRG4966...	-3	90	0.46	1
5	G1945	BM309016	BM309016 sak53e05.y1 Gm-c1036 Glycine max cD...	-3	91	0.46	1
5	G1945	BI958830	BI958830 HVSMEn0016M17f Hordeum vulgare rach...	-1	103	0.46	1
5	G1945	AY023671	AY023671 Oryza sativa microsatellite MRG5996...	3	90	0.46	1
5	G1945	AY022965	AY022965 Oryza sativa microsatellite MRG5290...	3	90	0.46	1
5	G1945	AY022966	AY022966 Oryza sativa microsatellite MRG5291...	3	90	0.46	1
5	G1945	AY023223	AY023223 Oryza sativa microsatellite MRG5548...	1	90	0.46	1
5	G1945	AY022337	AY022337 Oryza sativa microsatellite MRG4662...	-1	90	0.47	1
5	G1945	LSA17617	Y17617 Lactuca sativa SSR microsatellite seq...	-3	90	0.47	1
5	G1945	AY023539	AY023539 Oryza sativa microsatellite MRG5864...	2	90	0.47	1
5	G1945	BE398931	BE398931 WHE0028.A05F990514 ITEC WHE Wheat E...	-3	90	0.48	1
5	G1945	AW509821	AW509821 ga66a12.y1 Moss EST library PPU Phy...	-3	96	0.48	1
5	G1945	BF429199	BF429199 WHE1709_F06_K11ZS Wheat heat stress...	-3	92	0.49	1
5	G1945	BG323086	BG323086 EM1_14_G01.g1_A002 Embryo 1 (EM1) S...	-3	93	0.49	1
5	G1945	AW622868	AW622868 EST306938 tomato flower buds 3-8 mm...	2	89	0.5	1
5	G1945	AW060035	AW060035 660015F03.x1 660 - Mixed stages of ...	-2	100	0.5	1
5	G1945	AL370373	AL370373 MtBA37D08F1 MtBA Medicago truncatul...	-2	99	0.5	1
5	G1945	BF429042	BF429042 WHE1704_D08_H16ZS Wheat heat stress...	-2	92	0.51	1
5	G1945	BM417507	BM417507 952018C02.y1 952 - BMS tissue from ...	-2	90	0.51	1
5	G1945	BG604726	BG604726 WHE0941_E01_I01ZS Wheat 5-15 DAP sp...	-1	90	0.52	1
5	G1945	AV396249	AV396249 AV396249 Chlamydomonas reinhardtii ...	-1	99	0.53	1
5	G1945	BE591107	BE591107 WHE0861_B02_D03ZS Wheat 20-45 DAP s...	-3	90	0.53	1
5	G1945	BH126759	BH126759 BARC-Satt593 Size-selected soybean ...	-2	90	0.53	1
5	G1945	BE398712	BE398712 WHE0024.D06F990702 ITEC WHE Wheat E...	-3	90	0.53	1
5	G1945	BI126966	BI126966 I083P82P Populus leaf cDNA library ...	-3	90	0.54	1
5	G1945	MZEWXBA	M61192 Z.mays spontaneous deletion sequence ...	-3	90	0.54	1
5	G1945	AI637171	AI637171 603001G03.x1 603 - stressed root cD...	-3	102	0.55	1
5	G1945	AF143975	AF143975 Pinus taeda microsatellite PtTX3037...	-3	90	0.56	1
5	G1945	BE399960	BE399960 WHE0044.B09F990602 ITEC WHE Wheat E...	-2	90	0.57	1
5	G1945	VLA252882	AJ252882 Vitis labrusca VMC4D4 microsatellit...	-2	90	0.58	1
5	G1945	VVI252883	AJ252883 Vitis vinifera cv Syrah VMC4D4 micr...	-2	90	0.58	1
5	G1945	VVI252884	AJ252884 Vitis vinifera cv Cabernet Sauvigno...	-2	90	0.58	1
5	G1945	BG126055	BG126055 EST471701 tomato shoot/meristem Lyc...	-1	92	0.58	1

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5	G1945	BG463632	BG463632 EM1_50_A11.g1_A002 Embryo 1 (EM1) S...	2	91	0.58	1
5	G1945	BG262740	BG262740 WHE0940_F10_L20ZS Wheat 5-15 DAP sp...	-1	91	0.58	1
5	G1945	BE611882	BE611882 sr01b07.y1 Gm-c1049 Glycine max cDN...	1	97	0.58	1
5	G1945	AI563542	AI563542 EST00666 watermelon lambda zap libr...	-3	90	0.58	1
5	G1945	AI164563	AI164563 A065P06U Hybrid aspen plasmid libra...	-2	90	0.59	1
5	G1945	AV626112	AV626112 AV626112 Chlamydomonas reinhardtii ...	-1	90	0.6	1
5	G1945	VAM252876	AJ252876 Vitis amurensis VMC4D4 microsatelli...	-2	90	0.6	1
5	G1945	VBE252875	AJ252875 Vitis berlandieri VMC4D4 microsatel...	-2	90	0.6	1
5	G1945	VRI252873	AJ252873 Vitis riparia VMC4D4 microsatellite...	-2	90	0.6	1
5	G1945	VRO252874	AJ252874 Vitis rotundifolia VMC4D4 microsate...	-2	90	0.6	1
5	G1945	VRU252877	AJ252877 Vitis rupestris VMC4D4 microsatelli...	-2	90	0.6	1
5	G1945	VVI252878	AJ252878 Vitis vinifera cv Sultanina VMC4D4 ...	-2	90	0.6	1
5	G1945	BI472047	BI472047 sah98g04.y1 Gm-c1050 Glycine max cD...	-3	97	0.6	1
5	G1945	PQU252880	AJ252880 Parthenocissus quinquefolia VMC4D4 ...	-2	90	0.61	1
5	G1945	VAR252879	AJ252879 Vitis arizonica VMC4D4 microsatelli...	-2	90	0.61	1
5	G1945	BJ158144	BJ158144 BJ158144 full length cDNA library, ...	2	90	0.63	1
5	G1945	AI164229	AI164229 A057P61U Hybrid aspen plasmid libra...	-2	94	0.63	1
5	G1945	BF293975	BF293975 WHE2162_C12_F24ZS Triticum turgidum...	-3	90	0.64	1
5	G1945	GI-15528814	hypothetical protein~similar to Arabidopsi...	1	396	1.10E-36	1
5	G1945	GI-12643044	AC060755_3 putative AT-Hook DNA-binding pr...	1	241	4.70E-23	2
5	G1945	GI-4165183	SAP1 protein	1	219	4.60E-21	2
5	G1945	GI-5042445	AC007789_8 hypothetical protein	1	220	7.20E-17	1
5	G1945	GI-2213534	DNA-binding PD1-like protein	1	194	8.70E-14	1
5	G1945	GI-7488826	T06582 probable DNA-binding protein - gard...	1	194	8.70E-14	1
5	G1945	GI-2213536	DNA-binding protein PD1	1	194	1.00E-13	1
5	G1945	GI-7488825	T06584 probable DNA-binding protein - gard...	1	194	1.00E-13	1
5	G1945	GI-100214	S14971 extensin class I (clone wY) - tomato	1	52	0.022	2
5	G1945	GI-1345535	extensin (class I)	1	52	0.022	2
5	G1945	GI-8099121	hypothetical protein [Oryza sativa]	3	73	0.097	1
5	G1945	GI-13897322	somatic embryogenesis receptor-like kinase...	1	74	0.12	2
5	G1945	GI-21992	extensin	2	61	0.14	4
5	G1945	GI-81286	S22697 extensin - Volvox carteri (fragment)	2	61	0.14	4
5	G1945	GI-100216	S14975 extensin class II (clone uJ-2) - to...	2	55	0.19	2

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5	G1945	GI-1345538	extensin (class II)	2	55	0.19	2
5	G1945	GI-2108256	extensin	1	50	0.25	2
5	G1945	GI-6103625	unknown	2	74	0.28	2
5	G1945	GI-310925	cysteine-rich extensin-like protein-2	2	85	0.33	1
5	G1945	GI-539030	B48232 cysteine-rich extensin-like protein...	2	85	0.33	1
5	G1945	GI-6624712	this transcript covers in divergent orient...	-2	62	0.42	2
5	G1945	GI-4467884	extensin (class I)	2	49	0.48	3
5	G1945	GI-7488997	S14973 extensin class I (clone uG) - tomat...	2	49	0.48	3
5	G1945	GI-168237	hydroxyproline-rich protein	1	60	0.68	3
5	G1945	GI-445130	1908433A Hyp-rich glycoprotein [Helianthus...	1	60	0.68	3
5	G1945	GI-7442098	T12698 extensin - common sunflower	1	60	0.68	3
5	G1945	GI-100213	S14972 extensin class I (clone w6) - tomato	2	47	0.69	3
5	G1945	GI-1345536	extensin (class I)	2	47	0.69	3
5	G1945	GI-2129866	S59482 hydroxyproline-rich cell wall glyco...	2	41	0.71	2
5	G1945	GI-322760	PQ0474 pistil extensin-like protein precur...	-2	71	0.84	1
5	G1945	GI-19917	Pistil extensin like protein, partial CDS...	-2	71	0.87	1
5	G1945	GI-18844779	contains ESTs AU032297(R3855),(R3855)~unkn...	1	64	0.91	2
5	G1945	GI-6691125	AF213696_1 FH protein NFH2	2	84	0.94	2
5	G1945	GI-1486265	extensin	1	61	0.94	3
5	G1945	GI-7442095	T09965 extensin CYC17 precursor - Madagasc...	1	61	0.94	3
5	G1945	GI-435039	proline-rich cell wall protein	-2	78	0.96	1
5	G1945	GI-451544	proline-rich cell wall protein	-2	78	0.96	1
5	G1945	GI-7441828	T10737 extensin-like cell wall protein - s...	-2	78	0.96	1
5	G1945	GI-7441829	T09854 proline-rich cell wall protein - up...	-2	78	0.96	1
5	G1945	GI-2108258	extensin	-2	59	0.97	1
5	G1945	GI-6942015	extensin-like proline-rich protein RiP-5	-2	59	0.97	1
5	G1945	GI-6691123	AF213695_1 FH protein NFH1	2	73	0.97	2
5	G1945	GI-535586	proline rich protein	-2	74	0.98	2
5	G1945	GI-1084362	S53504 extensin-like protein S3 - alfalfa	-2	74	0.98	2
5	G1945	GI-9711862	putative extensin-like protein [Oryza sativa]	-2	83	0.98	1
5	G1945	GI-13161443	putative extensin-like protein [Oryza sativa]	-2	83	0.98	1
5	G1945	GI-169880	nodulin	-2	58	0.99	1
5	G1945	GI-311928	nodulin-45	2	58	0.99	1

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5	G1945	GI-421877	S34260 nodulin-45 - narrow-leaved blue lupine	2	58	0.99	1
5	G1945	GI-4324621	somatic regenerator RegA	-2	85	0.99	1
5	G1945	GI-4324623	somatic regenerator RegA	-2	85	0.99	1
5	G1945	GI-559557	arabinogalactan-protein	2	73	0.991	1
5	G1945	GI-397517	hydroxyproline-rich glycoprotein	2	57	0.997	1
5	G1945	GI-347457	hydroxyproline-rich glycoprotein	2	47	0.999	3
5	G1945	GI-688080	lectin=chitin-binding protein [Solanum tub...	-2	56	0.9993	1
5	G1945	GI-15290046	hypothetical protein [Oryza sativa]	2	75	0.9996	1
5	G1945	GI-310929	cysteine-rich extensin-like protein-4	2	72	0.9996	1
5	G1945	GI-13897310	SERK2 protein [Zea mays]	1	67	0.9996	2
5	G1945	GI-539032	D48232 cysteine-rich extensin-like protein...	2	72	0.9997	1
5	G1945	GI-99441	A33647 sulfated surface glycoprotein 185 -...	2	64	0.99991	2
5	G1945	GI-134920	SSGP_VOLCA SULFATED SURFACE GLYCOPROTEIN 1...	2	64	0.99991	2
5	G1945	GI-1405821	SULFATED SURFACE GLYCOPROTEIN 185	2	64	0.99991	2
7	G2155	BH480897	BH480897 BOGRA01TF BOGR Brassica oleracea ge...	-1	645	8.10E-61	1
7	G2155	BG646893	BG646893 EST508512 HOGA Medicago truncatula ...	2	540	8.80E-50	1
7	G2155	BG647027	BG647027 EST508646 HOGA Medicago truncatula ...	3	466	5.30E-42	1
7	G2155	BI426899	BI426899 sag08g12.y1 Gm-c1080 Glycine max cD...	1	441	3.40E-39	1
7	G2155	BF650426	BF650426 NF096G12EC1F1098 Elicited cell cult...	3	437	8.00E-39	1
7	G2155	AP004020	AP004020 Oryza sativa chromosome 2 clone OJ1...	2	440	2.40E-38	1
7	G2155	AW574000	AW574000 EST316591 GVN Medicago truncatula c...	1	423	2.30E-37	1
7	G2155	BI308126	BI308126 EST529536 GPOD Medicago truncatula ...	3	419	6.80E-37	1
7	G2155	BG647144	BG647144 EST508763 HOGA Medicago truncatula ...	1	418	6.90E-37	1
7	G2155	AW774484	AW774484 EST333635 KV3 Medicago truncatula c...	1	418	7.70E-37	1
7	G2155	AP003891	AP003891 Oryza sativa chromosome 8 clone OJ1...	2	418	5.20E-36	1
7	G2155	AP004587	AP004587 Oryza sativa chromosome 8 clone P05...	3	418	5.20E-36	1
7	G2155	BG581882	BG581882 EST483618 GVN Medicago truncatula c...	3	406	1.30E-35	1
7	G2155	BH566718	BH566718 BOHCV23TR BOHC Brassica oleracea ge...	-2	400	5.70E-35	1
7	G2155	BH510717	BH510717 BOGGW07TF BOGG Brassica oleracea ge...	1	399	8.60E-35	1
7	G2155	BE432188	BE432188 EST398717 tomato breaker fruit, TIG...	3	398	1.40E-34	1
7	G2155	OSJN00182	AL662981 Oryza sativa chromosome 4 clone OSJ...	1	404	1.60E-34	1
7	G2155	AP004165	AP004165 Oryza sativa chromosome 2 clone OJ1...	-3	400	4.20E-34	1
7	G2155	AP003526	AP003526 Oryza sativa chromosome 6 clone P05...	1	397	8.80E-34	1

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7	G2155	AP004757	AP004757 Oryza sativa chromosome 6 clone P06...	-3	389	6.20E-33	1
7	G2155	BG134451	BG134451 EST467343 tomato crown gall Lycoper...	1	379	1.30E-32	1
7	G2155	BH730050	BH730050 BOMEB22TF BO_2_3_KB Brassica olerac...	-1	377	1.40E-32	1
7	G2155	AW278127	AW278127 sf40a09.y1 Gm-c1009 Glycine max cDN...	1	379	1.50E-32	1
7	G2155	BH419879	BH419879 BOGGX69TF BOGG Brassica oleracea ge...	-2	376	1.90E-32	1
7	G2155	BM110212	BM110212 EST557748 potato roots Solanum tube...	1	375	2.70E-32	1
7	G2155	BI924382	BI924382 EST544271 tomato flower, buds 0-3 m...	3	376	3.20E-32	1
7	G2155	BH660108	BH660108 BOHVI48TF BO_2_3_KB Brassica olerac...	-1	373	3.80E-32	1
7	G2155	AP004635	AP004635 Oryza sativa chromosome 8 clone P06...	-2	379	7.10E-32	1
7	G2155	AP004698	AP004698 Oryza sativa chromosome 8 clone P04...	2	379	7.10E-32	1
7	G2155	BI699513	BI699513 sag37g08.y1 Gm-c1081 Glycine max cD...	2	372	8.30E-32	1
7	G2155	AL366947	AL366947 MtBA11B10F1 MtBA Medicago truncatul...	1	369	1.70E-31	1
7	G2155	BH550632	BH550632 BOGUC18TR BOGU Brassica oleracea ge...	-2	364	3.20E-31	1
7	G2155	BH729110	BH729110 BOHVN82TF BO_2_3_KB Brassica olerac...	-2	358	1.80E-30	1
7	G2155	BI971972	BI971972 sag84f09.y1 Gm-c1084 Glycine max cD...	1	358	2.30E-30	1
7	G2155	AV411735	AV411735 AV411735 Lotus japonicus young plan...	1	354	7.50E-30	1
7	G2155	AW596625	AW596625 sj14f10.y1 Gm-c1032 Glycine max cDN...	2	353	7.80E-30	1
7	G2155	AW980581	AW980581 EST391734 GVN Medicago truncatula c...	3	352	8.50E-30	1
7	G2155	BG583687	BG583687 EST485440 GVN Medicago truncatula c...	2	346	3.00E-29	1
7	G2155	BH717588	BH717588 BOMDB19TF BO_2_3_KB Brassica olerac...	2	343	7.60E-29	1
7	G2155	BH664974	BH664974 BOMBC11TF BO_2_3_KB Brassica olerac...	2	341	9.50E-29	1
7	G2155	AP003683	AP003683 Oryza sativa genomic DNA, chromosom...	3	347	1.70E-28	1
7	G2155	BG045781	BG045781 saa06a11.y1 Gm-c1058 Glycine max cD...	3	342	1.80E-28	1
7	G2155	BI321563	BI321563 saf12g07.y3 Gm-c1076 Glycine max cD...	1	337	3.70E-28	1
7	G2155	BH481983	BH481983 BOGYI73TR BOGY Brassica oleracea ge...	2	335	4.30E-28	1
7	G2155	BE203784	BE203784 EST396460 KV0 Medicago truncatula c...	2	337	4.50E-28	1
7	G2155	BH513264	BH513264 BOHQC93TR BOHQ Brassica oleracea ge...	-3	334	5.30E-28	1
7	G2155	BH596283	BH596283 BOGBL42TR BOGB Brassica oleracea ge...	2	333	7.20E-28	1
7	G2155	AW776082	AW776082 EST335147 DSIL Medicago truncatula ...	3	334	7.30E-28	1
7	G2155	BF004270	BF004270 EST432768 KV1 Medicago truncatula c...	3	333	1.20E-27	1
7	G2155	BE805340	BE805340 ss41d08.y1 Gm-c1061 Glycine max cDN...	1	332	1.80E-27	1
7	G2155	BH685875	BH685875 BOMBO90TR BO_2_3_KB Brassica olerac...	-1	327	3.80E-27	1
7	G2155	BF254863	BF254863 HVSMEf0005E05f Hordeum vulgare seed...	2	323	1.00E-26	1

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7	G2155	AW720668	AW720668 LjNEST14h9rc Lotus japonicus nodule...	1	322	1.30E-26	1
7	G2155	BH550963	BH550963 BOHQE85TR BOHQ Brassica oleracea ge...	-3	320	1.60E-26	1
7	G2155	AI960613	AI960613 sc86h10.y1 Gm-c1018 Glycine max cDN...	1	318	4.50E-26	1
7	G2155	BM526396	BM526396 sal40g01.y1 Gm-c1059 Glycine max cD...	3	317	5.10E-26	1
7	G2155	AW350603	AW350603 GM210008B10B12 Gm-r1021 Glycine max...	-1	315	5.90E-26	1
7	G2155	BI419871	BI419871 LjNEST17a9r Lotus japonicus nodule ...	2	316	8.20E-26	1
7	G2155	BF067277	BF067277 st37f11.y1 Gm-c1067 Glycine max cDN...	3	314	1.40E-25	1
7	G2155	BG881387	BG881387 sae81e03.y1 Gm-c1065 Glycine max cD...	3	307	5.90E-25	1
7	G2155	BM523502	BM523502 sam84f06.y2 Gm-c1087 Glycine max cD...	1	306	6.70E-25	1
7	G2155	AW774872	AW774872 EST334023 KV3 Medicago truncatula c...	3	306	1.00E-24	1
7	G2155	BH419964	BH419964 BOGQI28TF BOGQ Brassica oleracea ge...	-1	305	1.10E-24	1
7	G2155	BI701170	BI701170 sag55e11.y1 Gm-c1082 Glycine max cD...	2	303	1.40E-24	1
7	G2155	BH459056	BH459056 BOGKX90TR BOGK Brassica oleracea ge...	-2	300	2.20E-24	1
7	G2155	AW560824	AW560824 EST315872 DSIR Medicago truncatula ...	2	301	2.50E-24	1
7	G2155	BI972076	BI972076 sag85g11.y1 Gm-c1084 Glycine max cD...	2	300	3.10E-24	1
7	G2155	BH688757	BH688757 BOMDL66TF BO_2_3_KB Brassica olerac...	2	299	3.50E-24	1
7	G2155	BM779718	BM779718 EST590294 KV2 Medicago truncatula c...	-3	296	5.70E-24	1
7	G2155	BH669958	BH669958 BOMEJ12TF BO_2_3_KB Brassica olerac...	1	297	8.60E-24	1
7	G2155	AW761430	AW761430 sl67d09.y1 Gm-c1027 Glycine max cDN...	2	296	1.10E-23	1
7	G2155	BG583651	BG583651 EST485403 GVN Medicago truncatula c...	3	193	2.50E-23	2
7	G2155	AP004680	AP004680 Oryza sativa chromosome 6 clone OSJ...	-1	177	5.60E-23	2
7	G2155	AW621455	AW621455 EST312253 tomato root during/after ...	2	284	1.20E-22	1
7	G2155	AW349284	AW349284 GM210004B21H7 Gm-r1021 Glycine max ...	-2	280	2.90E-22	1
7	G2155	BE999313	BE999313 EST431036 GVSN Medicago truncatula ...	1	273	1.90E-21	1
7	G2155	BE998262	BE998262 EST429985 GVSN Medicago truncatula ...	2	270	4.70E-21	1
7	G2155	AI736668	AI736668 sb32a03.y1 Gm-c1012 Glycine max cDN...	2	262	3.10E-20	1
7	G2155	BJ203193	BJ203193 BJ203193 normalized full length cDN...	1	156	5.00E-20	2
7	G2155	BJ189956	BJ189956 BJ189956 normalized full length cDN...	3	259	6.20E-20	1
7	G2155	AW349908	AW349908 GM210006A20F9 Gm-r1021 Glycine max ...	-3	257	9.90E-20	1
7	G2155	AI494847	AI494847 sb06b09.y1 Gm-c1004 Glycine max cDN...	1	258	1.00E-19	1
7	G2155	AW780525	AW780525 sl72a07.y1 Gm-c1027 Glycine max cDN...	1	259	1.00E-19	1
7	G2155	BH430946	BH430946 BOHSM94TF BOHS Brassica oleracea ge...	-1	256	1.20E-19	1
7	G2155	BH679922	BH679922 BOMNO92TR BO_2_3_KB Brassica olerac...	3	254	1.60E-19	1

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7	G2155	AV422959	AV422959 AV422959 Lotus japonicus young plan...	2	256	1.70E-19	1
7	G2155	AV422634	AV422634 AV422634 Lotus japonicus young plan...	3	256	1.70E-19	1
7	G2155	BG465540	BG465540 RHIZ2_45_G09.b1_A003 Rhizome2 (RHIZ...	3	252	4.00E-19	1
7	G2155	BM525692	BM525692 sak62d03.y1 Gm-c1036 Glycine max cD...	1	251	4.60E-19	1
7	G2155	BI435896	BI435896 EST538657 P. infestans-challenged l...	3	252	5.80E-19	1
7	G2155	AI965992	AI965992 sc25a12.y1 Gm-c1013 Glycine max cDN...	3	250	5.90E-19	1
7	G2155	BE020549	BE020549 sm45a11.y1 Gm-c1028 Glycine max cDN...	3	247	2.10E-18	1
7	G2155	AW648634	AW648634 EST327184 tomato germinating seedli...	3	244	2.60E-18	1
7	G2155	BG599840	BG599840 EST504735 cSTS Solanum tuberosum cD...	2	150	3.20E-18	2
7	G2155	AW348874	AW348874 GM210010A10G1 Gm-r1021 Glycine max ...	-2	242	3.20E-18	1
7	G2155	BI974724	BI974724 sai72b06.y1 Gm-c1068 Glycine max cD...	1	243	3.30E-18	1
7	G2155	AP003938	AP003938 Oryza sativa chromosome 6 clone OJ1...	-2	249	4.30E-18	1
7	G2155	AP004303	AP004303 Oryza sativa chromosome 7 clone P04...	2	249	4.30E-18	1
7	G2155	AP003917	AP003917 Oryza sativa chromosome 8 clone OJ1...	3	156	5.80E-18	2
7	G2155	BG644865	BG644865 EST506484 KV3 Medicago truncatula c...	2	239	6.30E-18	1
7	G2155	BG600318	BG600318 EST505213 cSTS Solanum tuberosum cD...	1	243	6.30E-18	1
7	G2155	BF588135	BF588135 FM1_38_B09.b1_A003 Floral-Induced M...	3	238	1.20E-17	1
7	G2155	BE496294	BE496294 NXCI_022_C11_F NXCI (Nsf Xylem Comp...	1	234	3.50E-17	1
7	G2155	BG132224	BG132224 EST465116 tomato crown gall Lycoper...	2	232	5.60E-17	1
7	G2155	AW647786	AW647786 EST326240 tomato germinating seedli...	3	230	8.10E-17	1
7	G2155	AV415346	AV415346 AV415346 Lotus japonicus young plan...	3	231	8.60E-17	1
7	G2155	BI970749	BI970749 GM830011A20H08 Gm-r1083 Glycine max...	-1	228	1.00E-16	1
7	G2155	BI321153	BI321153 saf48b01.y3 Gm-c1077 Glycine max cD...	1	222	5.20E-16	1
7	G2155	AW672482	AW672482 LG1_360_E08.b1_A002 Light Grown 1 (...	3	222	5.60E-16	1
7	G2155	BE342838	BE342838 EST395682 potato stolon, Cornell Un...	1	221	6.70E-16	1
7	G2155	BH491363	BH491363 BOGPS71TR BOGP Brassica oleracea ge...	-1	219	8.30E-16	1
7	G2155	BE822274	BE822274 GM700017A10A4 Gm-r1070 Glycine max ...	-1	219	8.50E-16	1
7	G2155	AV933535	AV933535 AV933535 K. Sato unpublished cDNA l...	1	215	2.70E-15	1
7	G2155	AI522913	AI522913 sa91h08.y1 Gm-c1004 Glycine max cDN...	1	216	2.90E-15	1
7	G2155	BI406306	BI406306 159E11 Mature tuber lambda ZAP Sola...	1	215	3.00E-15	1
7	G2155	AW761107	AW761107 sl63c09.y1 Gm-c1027 Glycine max cDN...	1	217	3.00E-15	1
7	G2155	BG241750	BG241750 RHIZ2_50_G05.b1_A003 Rhizome2 (RHIZ...	3	215	3.80E-15	1
7	G2155	BI139442	BI139442 F131P74Y Populus flower cDNA librar...	-1	214	4.20E-15	1

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7	G2155	BH173434	BH173434 0104B13 maize genomic ORF library F...	-1	216	4.40E-15	1
7	G2155	BG589060	BG589060 EST490869 MHRP- Medicago truncatula...	1	209	1.00E-14	1
7	G2155	BH588550	BH588550 BOHOI48TR BOHO Brassica oleracea ge...	-2	209	1.20E-14	1
7	G2155	BE600816	BE600816 PI1_90_E07.b1_A002 Pathogen induced...	3	209	1.30E-14	1
7	G2155	BG593477	BG593477 EST492155 cSTS Solanum tuberosum cD...	3	208	1.70E-14	1
7	G2155	BG596340	BG596340 EST495018 cSTS Solanum tuberosum cD...	3	203	4.90E-14	1
7	G2155	BM322182	BM322182 PIC1_1_A05.b1_A002 Pathogen-infecte...	2	202	6.80E-14	1
7	G2155	BM322317	BM322317 PIC1_3_A06.b1_A002 Pathogen-infecte...	2	202	6.80E-14	1
7	G2155	BM322320	BM322320 PIC1_3_A09.b1_A002 Pathogen-infecte...	2	202	7.10E-14	1
7	G2155	BM322319	BM322319 PIC1_3_A08.b1_A002 Pathogen-infecte...	2	202	7.50E-14	1
7	G2155	BF324870	BF324870 su17c07.y1 Gm-c1066 Glycine max cDN...	1	202	8.90E-14	1
7	G2155	BM322185	BM322185 PIC1_1_A08.b1_A002 Pathogen-infecte...	2	202	9.10E-14	1
7	G2155	BM322192	BM322192 PIC1_1_B08.b1_A002 Pathogen-infecte...	2	202	9.10E-14	1
7	G2155	BM322318	BM322318 PIC1_3_A07.b1_A002 Pathogen-infecte...	2	202	9.10E-14	1
7	G2155	BG441060	BG441060 GA__Ea0011I19f Gossypium arboreum 7...	3	199	1.00E-13	1
7	G2155	AP003074	AP003074 Oryza sativa genomic DNA, chromosom...	-1	206	1.50E-13	1
7	G2155	AC007789	AC007789 Oryza sativa BAC OSJNBa0049B20 geno...	-1	206	1.50E-13	1
7	G2155	BE445433	BE445433 WHE1136_A09_B18ZS Wheat etiolated s...	2	199	1.60E-13	1
7	G2155	BE609898	BE609898 sq46e12.y1 Gm-c1019 Glycine max cDN...	3	199	1.60E-13	1
7	G2155	PSDBLPPD1	X98739 P.sativum mRNA encoding DNA-binding P...	1	202	1.70E-13	1
7	G2155	BE442709	BE442709 WHE1105_B09_C17ZS Wheat etiolated s...	3	198	2.00E-13	1
7	G2155	BI786439	BI786439 sai49b05.y1 Gm-c1065 Glycine max cD...	1	197	2.70E-13	1
7	G2155	BE600623	BE600623 PI1_89_D08.b1_A002 Pathogen induced...	3	197	2.90E-13	1
7	G2155	AMA132349	AJ132349 Antirrhinum majus mRNA for SAP1 pro...	3	198	3.10E-13	1
7	G2155	AI522924	AI522924 sa92b03.y1 Gm-c1004 Glycine max cDN...	2	197	3.20E-13	1
7	G2155	BE643892	BE643892 NXCI_048_F12_F NXCI (Nsf Xylem Comp...	3	197	3.40E-13	1
7	G2155	BM094108	BM094108 sah25e08.y1 Gm-c1036 Glycine max cD...	1	195	4.60E-13	1
7	G2155	BG651836	BG651836 sad61f05.y1 Gm-c1051 Glycine max cD...	3	195	4.70E-13	1
7	G2155	PSDBPPD1	X98738 P.sativum mRNA encoding DNA-binding p...	1	199	4.80E-13	1
7	G2155	AW455702	AW455702 707090A08.x1 707 - Mixed adult tiss...	3	194	4.90E-13	1
7	G2155	BE496149	BE496149 WHE1262_H03_P06ZS Secale cereale an...	2	195	5.00E-13	1
7	G2155	BM086350	BM086350 sah38h08.y1 Gm-c1036 Glycine max cD...	3	194	5.20E-13	1
7	G2155	AW928863	AW928863 EST337651 tomato flower buds 8 mm t...	3	193	6.80E-13	1

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7	G2155	AW448258	AW448258 BRY_1522 BRY Triticum aestivum cDNA...	3	191	7.40E-13	1
7	G2155	BM322184	BM322184 PIC1_1_A07.b1_A002 Pathogen-infecte...	2	194	7.80E-13	1
7	G2155	BI946361	BI946361 01104 leafy spurge Lambda HybriZAP ...	1	192	7.90E-13	1
7	G2155	BG350206	BG350206 084D10 Mature tuber lambda ZAP Sola...	3	190	1.10E-12	1
7	G2155	BI972355	BI972355 sag90d06.y1 Gm-c1084 Glycine max cD...	2	191	1.10E-12	1
7	G2155	D42950	D42950 D42950 Rice callus cDNA (H.Uchimiya) ...	2	192	1.20E-12	1
7	G2155	BM173594	BM173594 900948 Avicennia marina leaf cDNA L...	2	194	1.20E-12	1
7	G2155	AW622329	AW622329 EST313127 tomato root during/after ...	2	190	1.60E-12	1
7	G2155	BE442615	BE442615 WHE1101_G09_M17ZS Wheat etiolated s...	2	188	2.30E-12	1
7	G2155	BE555817	BE555817 sp94c01.y1 Gm-c1045 Glycine max cDN...	3	188	2.40E-12	1
7	G2155	BE330349	BE330349 so77e09.y1 Gm-c1040 Glycine max cDN...	3	188	2.50E-12	1
7	G2155	BI788210	BI788210 sag68a10.y1 Gm-c1082 Glycine max cD...	3	187	2.80E-12	1
7	G2155	AP004319	AP004319 Oryza sativa chromosome 1 clone B10...	2	192	4.70E-12	1
7	G2155	AW776953	AW776953 EST336018 DSIL Medicago truncatula ...	2	183	7.20E-12	1
7	G2155	AL508367	AL508367 AL508367 Hordeum vulgare Barke deve...	3	182	8.50E-12	1
7	G2155	BF187248	BF187248 EST443535 potato stolon, Cornell Un...	2	182	1.10E-11	1
7	G2155	AW066510	AW066510 660015F03.y1 660 - Mixed stages of ...	1	182	1.10E-11	1
7	G2155	AW596434	AW596434 sj12d05.y1 Gm-c1032 Glycine max cDN...	2	183	1.10E-11	1
7	G2155	BH732637	BH732637 BOMBI03TF BO_2_3_KB Brassica olerac...	2	180	1.30E-11	1
7	G2155	AV917319	AV917319 AV917319 K. Sato unpublished cDNA I...	2	178	2.30E-11	1
7	G2155	BI074657	BI074657 IP1_14_F04.b1_A002 Immature pannicl...	1	178	2.40E-11	1
7	G2155	BE591277	BE591277 WHE1655-1658_J17_J17ZS Wheat heat s...	1	178	2.50E-11	1
7	G2155	BI266587	BI266587 NF099D09IN1F1078 Insect herbivory M...	2	177	2.90E-11	1
7	G2155	BM371214	BM371214 EBro04_SQ003_M20_R IGF Barley EBro0...	2	179	2.90E-11	1
7	G2155	BG240061	BG240061 OV1_17_D10.b1_A002 Ovary 1 (OV1) So...	1	177	3.30E-11	1
7	G2155	BG240043	BG240043 OV1_17_B12.b1_A002 Ovary 1 (OV1) So...	1	177	3.50E-11	1
7	G2155	BI929403	BI929403 EST549292 tomato flower, 3 - 8 mm b...	1	175	3.70E-11	1
7	G2155	BG240220	BG240220 OV1_19_D02.b1_A002 Ovary 1 (OV1) So...	1	177	4.40E-11	1
7	G2155	BM136003	BM136003 WHE2604_D04_H08ZS Wheat Fusarium gr...	-1	174	6.30E-11	1
7	G2155	AV410107	AV410107 AV410107 Lotus japonicus young plan...	2	176	6.60E-11	1
7	G2155	BF429428	BF429428 WHE1803_A09_B17ZS Secale cereale an...	1	175	7.00E-11	1
7	G2155	AW132605	AW132605 se06d10.y1 Gm-c1013 Glycine max cDN...	3	174	7.20E-11	1
7	G2155	BE807468	BE807468 ss22h03.y1 Gm-c1047 Glycine max cDN...	2	175	7.50E-11	1

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7	G2155	BH596271	BH596271 BOGBL42TF BOGB Brassica oleracea ge...	-3	171	1.00E-10	1
7	G2155	AW906401	AW906401 EST342523 potato stolon, Cornell Un...	2	172	1.30E-10	1
7	G2155	AI881841	AI881841 606074A03.y1 606 - Ear tissue cDNA ...	3	171	1.30E-10	1
7	G2155	BE586257	BE586257 WHE501_B07_C13ZR Secale cereale alu...	2	171	1.40E-10	1
7	G2155	BF637181	BF637181 NF050F02LF1F1016 Developing leaf Me...	3	171	1.40E-10	1
7	G2155	AW755831	AW755831 sl09h02.y1 Gm-c1036 Glycine max cDN...	3	172	1.50E-10	1
7	G2155	BG352828	BG352828 sab91g04.y1 Gm-c1040 Glycine max cD...	3	171	1.60E-10	1
7	G2155	AW099294	AW099294 sd37h01.y1 Gm-c1016 Glycine max cDN...	2	173	1.80E-10	1
7	G2155	AW979681	AW979681 EST341290 tomato root deficiency, C...	1	169	2.30E-10	1
7	G2155	BF258208	BF258208 HVSMEf0015B16f Hordeum vulgare seed...	2	167	2.80E-10	1
7	G2155	AL373204	AL373204 MtBA56C11F1 MtBA Medicago truncatul...	3	169	2.80E-10	1
7	G2155	BH650598	BH650598 BOHZR58TR BO_2_3_KB Brassica olerac...	1	167	3.40E-10	1
7	G2155	BG583795	BG583795 EST485550 GVN Medicago truncatula c...	1	166	3.60E-10	1
7	G2155	BF636643	BF636643 NF091G07DT1F1055 Drought Medicago t...	1	165	7.00E-10	1
7	G2155	BF587149	BF587149 FM1_32_G07.b1_A003 Floral-Induced M...	3	164	1.00E-09	1
7	G2155	AV424890	AV424890 AV424890 Lotus japonicus young plan...	3	164	1.00E-09	1
7	G2155	BG130143	BG130143 EST475789 tomato shoot/meristem Lyc...	1	162	1.30E-09	1
7	G2155	BM094106	BM094106 sah25e06.y1 Gm-c1036 Glycine max cD...	1	161	1.80E-09	1
7	G2155	AI897688	AI897688 EST267131 tomato ovary, TAMU Lycope...	3	160	2.30E-09	1
7	G2155	AI988292	AI988292 sc98f12.y1 Gm-c1020 Glycine max cDN...	2	158	3.20E-09	1
7	G2155	AL372048	AL372048 MtBA48C06F1 MtBA Medicago truncatul...	1	159	4.10E-09	1
7	G2155	BE639390	BE639390 946024E11.y1 946 - tassel primordiu...	1	154	8.00E-09	1
7	G2155	BM079070	BM079070 MEST88-H11.T3 ISUM4-TN Zea mays cDN...	-1	160	1.10E-08	1
7	G2155	BM412174	BM412174 EST586501 tomato breaker fruit Lyco...	1	156	1.40E-08	1
7	G2155	BI699401	BI699401 sag36e12.y1 Gm-c1081 Glycine max cD...	1	153	1.50E-08	1
7	G2155	BG909764	BG909764 TaLr1108d02R TaLr1 Triticum aestivu...	3	152	1.60E-08	1
7	G2155	BM524672	BM524672 sal18d07.y1 Gm-c1059 Glycine max cD...	2	150	2.40E-08	1
7	G2155	BM524654	BM524654 sal18b12.y1 Gm-c1059 Glycine max cD...	2	150	2.50E-08	1
7	G2155	BM405827	BM405827 EST580154 potato roots Solanum tube...	2	150	3.20E-08	1
7	G2155	AV423934	AV423934 AV423934 Lotus japonicus young plan...	3	150	3.30E-08	1
7	G2155	BG599554	BG599554 EST504449 cSTS Solanum tuberosum cD...	2	157	4.70E-08	1
7	G2155	AW755604	AW755604 sl05h07.y1 Gm-c1036 Glycine max cDN...	3	147	4.80E-08	1
7	G2155	BE357932	BE357932 DG1_23_D12.b1_A002 Dark Grown 1 (DG...	1	146	6.10E-08	1

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7	G2155	BJ158045	BJ158045 BJ158045 full length cDNA library, ...	-3	146	6.60E-08	1
7	G2155	BE202989	BE202989 EST403011 KV1 Medicago truncatula c...	-3	146	6.60E-08	1
7	G2155	BE444180	BE444180 WHE1128_B06_D12ZS Wheat etiolated s...	2	146	7.10E-08	1
7	G2155	BM521838	BM521838 sak76f11.y1 Gm-c1036 Glycine max cD...	2	145	8.00E-08	1
7	G2155	BE125776	BE125776 DG1_57_B07.b1_A002 Dark Grown 1 (DG...	1	146	8.60E-08	1
7	G2155	BE587763	BE587763 WHE0652_C06_E12ZM Secale cereale ro...	1	144	1.20E-07	1
7	G2155	AW760534	AW760534 sl51e09.y1 Gm-c1027 Glycine max cDN...	1	143	1.30E-07	1
7	G2155	BE587194	BE587194 WHE0519_B07_D13ZR Secale cereale al...	1	145	1.50E-07	1
7	G2155	BI096714	BI096714 949019H11.y1 949 - Juvenile leaf an...	2	142	1.80E-07	1
7	G2155	AW309814	AW309814 sf25b03.x1 Gm-c1028 Glycine max cDN...	-1	151	1.90E-07	1
7	G2155	BI469296	BI469296 sai10a11.y1 Gm-c1053 Glycine max cD...	3	141	2.70E-07	1
7	G2155	AU198263	AU198263 AU198263 Rice green shoot Oryza sat...	1	141	2.70E-07	1
7	G2155	BF625927	BF625927 HVSMEa0014H11f Hordeum vulgare seed...	1	140	3.40E-07	1
7	G2155	BM441160	BM441160 EBed02_SQ002_J15_R IGF Barley EBed0...	1	138	5.20E-07	1
7	G2155	BH439306	BH439306 BOHGL38TR BOHG Brassica oleracea ge...	1	138	5.30E-07	1
7	G2155	BI430562	BI430562 949057A04.y1 949 - Juvenile leaf an...	1	143	5.90E-07	1
7	G2155	BG888793	BG888793 EST514644 cSTD Solanum tuberosum cD...	3	150	6.20E-07	1
7	G2155	BE923621	BE923621 EST427390 potato leaves and petiole...	1	137	8.10E-07	1
7	G2155	AI487942	AI487942 EST246264 tomato ovary, TAMU Lycope...	1	137	1.40E-06	1
7	G2155	BM307331	BM307331 sak27h05.y1 Gm-c1075 Glycine max cD...	1	134	1.60E-06	1
7	G2155	AV425818	AV425818 AV425818 Lotus japonicus young plan...	3	134	2.10E-06	1
7	G2155	AW031261	AW031261 EST274636 tomato callus, TAMU Lycop...	1	141	3.70E-06	1
7	G2155	BI932139	BI932139 EST552028 tomato flower, 8 mm to pr...	1	143	5.50E-06	1
7	G2155	BG510489	BG510489 sac78f02.y1 Gm-c1072 Glycine max cD...	3	133	8.80E-06	1
7	G2155	D15459	D15459 RICC0669A Rice callus Oryza sativa cD...	1	129	9.70E-06	1
7	G2155	AV421337	AV421337 AV421337 Lotus japonicus young plan...	2	129	1.20E-05	1
7	G2155	AW164140	AW164140 Ljirnpest20-626-g4 Ljirnp Lambda Hy...	1	127	1.40E-05	1
7	G2155	AW620872	AW620872 sj47g06.y1 Gm-c1033 Glycine max cDN...	3	125	2.30E-05	1
7	G2155	BI931107	BI931107 EST550996 tomato flower, 8 mm to pr...	1	136	2.40E-05	1
7	G2155	AI443215	AI443215 sa45h07.y1 Gm-c1004 Glycine max cDN...	1	125	2.50E-05	1
7	G2155	AW310124	AW310124 sf31d10.x1 Gm-c1028 Glycine max cDN...	-1	135	2.80E-05	1
7	G2155	BG040551	BG040551 NXSI_112_D08_F NXSI (Nsf Xylem Side...	1	124	3.00E-05	1
7	G2155	AW773742	AW773742 EST332728 KV3 Medicago truncatula c...	3	132	4.40E-05	1

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7	G2155	BG275315	BG275315 NXSI_142_D09_F NXSI (Nsf Xylem Side...	3	124	4.50E-05	1
7	G2155	BI928278	BI928278 EST548167 tomato flower, 3 - 8 mm b...	1	136	4.50E-05	1
7	G2155	BI929489	BI929489 EST549378 tomato flower, 3 - 8 mm b...	1	136	4.90E-05	1
7	G2155	AW720136	AW720136 LjNEST14h9r Lotus japonicus nodule ...	1	122	5.60E-05	1
7	G2155	BE923864	BE923864 EST427633 potato leaves and petiole...	1	120	8.60E-05	1
7	G2155	BJ186205	BJ186205 BJ186205 normalized full length cDN...	1	129	0.0001	1
7	G2155	AW773741	AW773741 EST332727 KV3 Medicago truncatula c...	3	128	0.00012	1
7	G2155	AI779587	AI779587 EST260466 tomato susceptible, Corne...	1	129	0.00013	1
7	G2155	BI927526	BI927526 EST547415 tomato flower, 3 - 8 mm b...	3	131	0.00015	1
7	G2155	BG239709	BG239709 sab74e11.y1 Gm-c1032 Glycine max cD...	3	127	0.00023	1
7	G2155	BG582457	BG582457 EST484202 GVN Medicago truncatula c...	3	116	0.00029	1
7	G2155	BG594217	BG594217 EST492895 cSTS Solanum tuberosum cD...	2	127	0.0003	1
7	G2155	BG592977	BG592977 EST491655 cSTS Solanum tuberosum cD...	-2	126	0.00039	1
7	G2155	BM407572	BM407572 EST581899 potato roots Solanum tube...	1	127	0.00045	1
7	G2155	BI675167	BI675167 949079C12.x2 949 - Juvenile leaf an...	-2	123	0.00089	1
7	G2155	BF639276	BF639276 NF011F11IN1F1092 Insect herbivory M...	2	123	0.0014	1
7	G2155	AP004116	AP004116 Oryza sativa chromosome 2 clone OJ1...	1	126	0.0025	1
7	G2155	AW929149	AW929149 EST337937 tomato flower buds 8 mm t...	2	119	0.0044	1
7	G2155	AL383224	AL383224 MtBC12G03F1 MtBC Medicago truncatul...	2	106	0.0048	1
7	G2155	BJ196157	BJ196157 BJ196157 normalized full length cDN...	1	106	0.0051	1
7	G2155	BG601044	BG601044 EST505939 cSTS Solanum tuberosum cD...	1	115	0.0093	1
7	G2155	BM299690	BM299690 MCR053G12_23908 Ice plant Lambda Un...	2	116	0.0099	1
7	G2155	AI691406	AI691406 606015E08.x1 606 - Ear tissue cDNA ...	-1	115	0.012	1
7	G2155	AW216305	AW216305 687047G05.x1 687 - Early embryo fro...	-2	113	0.016	1
7	G2155	BM093021	BM093021 saj04a05.y1 Gm-c1065 Glycine max cD...	3	110	0.017	1
7	G2155	BM112694	BM112694 EST560230 potato roots Solanum tube...	1	114	0.022	1
7	G2155	ZDZEAR260	X53609 Z.diploperennis repetitive DNA (clone...	-2	98	0.045	1
7	G2155	BI934755	BI934755 EST554644 tomato flower, anthesis L...	2	111	0.046	1
7	G2155	BM308752	BM308752 sak50a05.y1 Gm-c1036 Glycine max cD...	1	108	0.059	1
7	G2155	AP003925	AP003925 Oryza sativa chromosome 8 clone OJ1...	-2	113	0.076	1
7	G2155	AP004562	AP004562 Oryza sativa chromosome 8 clone P04...	-1	113	0.076	1
7	G2155	AI726212	AI726212 BNLGHi5295 Six-day Cotton fiber Gos...	-2	111	0.087	1
7	G2155	D43486	D43486 D43486 Rice callus cDNA (H.Uchimiya) ...	3	95	0.11	1

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7	G2155	AL375620	AL375620 MtBB15H05F1 MtBB Medicago truncatul...	1	103	0.14	1
7	G2155	BF257835	BF257835 HVSMEf0014A01f Hordeum vulgare seed...	2	105	0.15	1
7	G2155	AZ126664	AZ126664 OSJNBb0078L18r CUGI Rice BAC Librar...	2	106	0.15	1
7	G2155	BI643921	BI643921 NXPV_129_D06_F NXPV (Nsf Xylem Plan...	1	93	0.18	1
7	G2155	BG848679	BG848679 1024022E01.x1 C. reinhardtii CC-169...	-3	108	0.18	1
7	G2155	BI788421	BI788421 sag70e10.y1 Gm-c1082 Glycine max cD...	3	100	0.25	1
7	G2155	BG851510	BG851510 1024031E06.x2 C. reinhardtii CC-169...	-3	106	0.3	1
7	G2155	BE446692	BE446692 WHE1139_D09_H17ZS Wheat etiolated s...	2	97	0.3	1
7	G2155	AI494984	AI494984 sa93e04.y1 Gm-c1004 Glycine max cDN...	1	89	0.32	1
7	G2155	AI494991	AI494991 sa93f04.y1 Gm-c1004 Glycine max cDN...	2	89	0.35	1
7	G2155	BI948051	BI948051 HVSMEI0008A05f Hordeum vulgare spik...	-3	103	0.42	1
7	G2155	AI441147	AI441147 sa59d03.y1 Gm-c1004 Glycine max cDN...	3	91	0.44	1
7	G2155	AU183195	AU183195 AU183195 Rice immature leaf includi...	1	97	0.44	1
7	G2155	BM444822	BM444822 EBem09_SQ006_J09_R IGF Barley EBem0...	1	89	0.45	1
7	G2155	BM112790	BM112790 EST560326 potato roots Solanum tube...	3	100	0.46	1
7	G2155	AI494950	AI494950 sa93a09.y1 Gm-c1004 Glycine max cDN...	1	89	0.47	1
7	G2155	AZ917746	AZ917746 1006001H12.y1 1006 - RescueMu Grid ...	-1	97	0.48	1
7	G2155	BH599467	BH599467 BOGNL80TF BOGN Brassica oleracea ge...	3	102	0.5	1
7	G2155	AZ917748	AZ917748 1006001H12.y2 1006 - RescueMu Grid ...	-1	97	0.52	1
7	G2155	AI637171	AI637171 603001G03.x1 603 - stressed root cD...	-3	100	0.58	1
7	G2155	BH129197	BH129197 G-4I5 Maize Random Small-insert Gen...	-3	101	0.6	1
7	G2155	BE611882	BE611882 sr01b07.y1 Gm-c1049 Glycine max cDN...	1	95	0.67	1
7	G2155	AQ794411	AQ794411 nbxb0053A19f CUGI Rice BAC Library ...	3	98	0.85	1
7	G2155	AW622868	AW622868 EST306938 tomato flower buds 3-8 mm...	2	83	0.88	1
7	G2155	AC026758	AC026758 Oryza sativa chromosome 10 BAC OSJN...	2	100	0.9	1
7	G2155	AU091426	AU091426 AU091426 Rice cDNA from immature le...	-1	85	0.94	1
7	G2155	AI460865	AI460865 sa70c03.y1 Gm-c1004 Glycine max cDN...	3	92	0.95	1
7	G2155	BH023348	BH023348 GH_MBb0004I22f Gossypium hirsutum L...	2	95	0.95	1
7	G2155	BG418060	BG418060 HVSMEk0021C01f Hordeum vulgare test...	3	96	0.97	1
7	G2155	BI643533	BI643533 949079C12.x1 949 - Juvenile leaf an...	-3	94	0.97	1
7	G2155	BM309583	BM309583 sak64c09.y1 Gm-c1036 Glycine max cD...	1	93	0.992	1
7	G2155	BM377393	BM377393 EBem04_SQ003_A02_R IGF Barley EBem0...	2	90	0.995	1
7	G2155	BF274574	BF274574 GA__Eb0021G20f Gossypium arboreum 7...	3	92	0.998	1

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7	G2155	BG323043	BG323043 EM1_14_C04.g1_A002 Embryo 1 (EM1) S...	2	91	0.999	1
7	G2155	BH426755	BH426755 BOHGA51TR BOHG Brassica oleracea ge...	-2	93	0.9995	1
7	G2155	BG049445	BG049445 OV1_20_A09.g1_A002 Ovary 1 (OV1) So...	1	91	0.9996	1
7	G2155	BI974612	BI974612 sai70g08.y1 Gm-c1068 Glycine max cD...	3	91	0.9997	1
7	G2155	BI267267	BI267267 NF100C06IN1F1070 Insect herbivory M...	2	92	0.9998	1
7	G2155	OSJN00107	AL606729 Oryza sativa chromosome 4 clone OSJ...	-2	95	0.9998	1
7	G2155	BG858008	BG858008 1024055C06.y1 C. reinhardtii CC-169...	-2	93	0.99992	1
7	G2155	BG649667	BG649667 RHIZ2_82_C04.b1_A003 Rhizome2 (RHIZ...	1	90	0.99993	1
7	G2155	BE025350	BE025350 945025C05.Y1 945 - Mixed adult tiss...	-1	90	0.99993	1
7	G2155	AZ126644	AZ126644 OSJNBb0078P23r CUGI Rice BAC Librar...	-3	92	0.99995	1
7	G2155	GI-15528814	hypothetical protein~similar to Arabidopsi...	1	347	1.80E-31	1
7	G2155	GI-12643044	AC060755_3 putative AT-Hook DNA-binding pr...	1	250	6.60E-21	1
7	G2155	GI-4165183	SAP1 protein	1	198	1.70E-19	2
7	G2155	GI-2213534	DNA-binding PD1-like protein	1	202	7.30E-16	1
7	G2155	GI-7488826	T06582 probable DNA-binding protein - gard...	1	202	7.30E-16	1
7	G2155	GI-2213536	DNA-binding protein PD1	1	199	2.00E-15	1
7	G2155	GI-7488825	T06584 probable DNA-binding protein - gard...	1	199	2.00E-15	1
7	G2155	GI-5042445	AC007789_8 hypothetical protein	1	206	2.30E-15	1
7	G2155	GI-100214	S14971 extensin class I (clone wY) - tomato	-2	49	0.12	2
7	G2155	GI-1345535	extensin (class I)	-2	49	0.12	2
7	G2155	GI-4467884	extensin (class I)	-2	52	0.16	2
7	G2155	GI-7488997	S14973 extensin class I (clone uG) - tomat...	-2	52	0.16	2
7	G2155	GI-72327	ZMZM5 glutelin 5 - maize	2	46	0.2	2
7	G2155	GI-3808062	PV100	-3	90	0.47	1
7	G2155	GI-11357142	T44430 protein PV100 [imported] - winter s...	-3	90	0.47	1
7	G2155	GI-15217275	AC078944_30 Hypothetical protein [Oryza sa...	2	82	0.54	1
7	G2155	GI-13486758	hypothetical protein [Oryza sativa]	-3	84	0.58	1
7	G2155	GI-18568237	AF466203_3 putative orf1 [Zea mays]	-1	78	0.61	1
7	G2155	GI-609288	orf1	-1	77	0.74	1
7	G2155	GI-1076786	S52246 hypothetical protein 1 - perennial ...	-1	77	0.74	1
7	G2155	GI-1588259	2208274A ORF [Zea diploperennis]	-1	77	0.74	1
7	G2155	GI-2130116	JC4641 transposable retroelement homologue...	-1	77	0.74	1
7	G2155	GI-2108256	extensin	-2	56	0.84	2

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7	G2155	GI-11034617	hypothetical protein~similar to Oryza sati...	-2	61	0.96	2
7	G2155	GI-14090217	hypothetical protein~similar to Oryza sati...	-2	61	0.96	2
7	G2155	GI-459269	transcribed sequence 1087	-2	77	0.96	1
7	G2155	GI-542190	S42933 hypothetical protein 1087 - maize	-2	77	0.96	1
7	G2155	GI-14164447	hypothetical protein [Oryza sativa]	-1	57	0.96	2
7	G2155	GI-4666360	AF119050_1 zinc-finger protein 1	-1	77	0.98	1
7	G2155	GI-1617471	ORFI	-1	72	0.99	1
7	G2155	GI-17154773	AF104392_1 extensin-like protein [Cucumis ...	2	59	0.993	2
7	G2155	GI-2108258	extensin	-2	56	0.995	1
7	G2155	GI-12328465	hypothetical protein [Oryza sativa]	3	55	0.999	1
7	G2155	GI-18461282	hypothetical protein [Oryza sativa]	-1	71	0.9996	1
7	G2155	GI-2129873	S67502 ABR18 protein - garden pea	2	54	0.9999	1

What is claimed is:

1. An isolated or recombinant polynucleotide comprising a nucleotide sequence encoding a polypeptide having an amino acid sequence of SEQ ID NO: 2 (G1073), SEQ ID NO: 4 (G2789), SEQ ID NO: 6 (G1945) or SEQ ID NO: 8 (G2155), or a complementary nucleotide sequence thereof.

2. A transgenic plant, which plant comprises a recombinant polynucleotide comprising a nucleotide sequence from the group consisting of:

(a) a nucleotide sequence encoding a polypeptide comprising a sequence selected from SEQ ID NO: 2, 4, 6 and 8, or a complementary nucleotide sequence thereof;

(b) a nucleotide sequence encoding a polypeptide comprising a conservatively substituted variant of a polypeptide of (a);

(c) a nucleotide sequence comprising a sequence selected from those of SEQ ID NO: 1, 3, 5 and 7, or a complementary nucleotide sequence thereof;

(d) a nucleotide sequence comprising silent substitutions in a nucleotide sequence of (c);

(e) a nucleotide sequence which hybridizes under stringent conditions to a nucleotide sequence of one or more of: (a), (b), (c), or (d);

(f) a nucleotide sequence comprising at least 15 consecutive nucleotides of a sequence of any of (a)-(e);

(g) a nucleotide sequence comprising a subsequence or fragment of any of (a)-(f), which subsequence or fragment encodes a polypeptide having a biological activity that modifies a plant's biomass;

(h) a nucleotide sequence having at least 40% sequence identity to a nucleotide sequence of any of (a)-(g);

(i) a nucleotide sequence having at least 85% sequence identity to a nucleotide sequence of any of (a)-(g);

(j) a nucleotide sequence which encodes a polypeptide having at least 40% sequence identity to a polypeptide of SEQ ID NO: 2, 4, 6 or 8;

(k) a nucleotide sequence which encodes a polypeptide having at least 85% sequence identity to a polypeptide of SEQ ID NO: 2, 4, 6 or 8;

(l) a nucleotide sequence which encodes a polypeptide containing a conserved domain having at least 65% sequence identity to a conserved domain of a polypeptide of SEQ ID NO: 2, 4, 6, or 8;

(m) a nucleotide sequence which encodes a plant transcription factor comprising a fragment having 6 consecutive amino acids from a region of SEQ ID NO: 2, 4, 6, or 8 outside of the conserved domain;

(n) a nucleotide sequence having at least 85% sequence identity to (m);

(o) a nucleotide sequence which encodes a plant transcription factor comprising a fragment having 8 consecutive amino acids from a region of SEQ ID NO: 2, 4, 6, or 8 outside of the conserved domain; and

(p) a nucleotide sequence having at least 85% sequence identity to (o).

3. The transgenic plant of claim 2, further comprising a constitutive, inducible, or tissue-specific promoter operably linked to said nucleotide sequence.

4. An isolated or recombinant polynucleotide comprising a nucleotide sequence from the group consisting of:

(a) a nucleotide sequence encoding a polypeptide comprising a sequence selected from SEQ ID NO: 2, 4, 6 and 8, or a complementary nucleotide sequence thereof;

(b) a nucleotide sequence encoding a polypeptide comprising a conservatively substituted variant of a polypeptide of (a);

(c) a nucleotide sequence comprising a sequence selected from those of SEQ ID NO: 1, 3, 5 and 7, or a complementary nucleotide sequence thereof;

(d) a nucleotide sequence comprising silent substitutions in a nucleotide sequence of (c);

(e) a nucleotide sequence which hybridizes under stringent conditions to a nucleotide sequence of one or more of: (a), (b), (c), or (d);

(f) a nucleotide sequence comprising at least 15 consecutive nucleotides of a sequence of any of (a)-(e);

(g) a nucleotide sequence comprising a subsequence or fragment of any of (a)-(f), which subsequence or fragment encodes a polypeptide having a biological activity that modifies a plant's biomass;

(h) a nucleotide sequence having at least 40% sequence identity to a nucleotide sequence of any of (a)-(g);

(i) a nucleotide sequence having at least 85% sequence identity to a nucleotide sequence of any of (a)-(g);

(j) a nucleotide sequence which encodes a polypeptide having at least 40% sequence identity to a polypeptide of SEQ ID NO: 2, 4, 6 or 8;

(k) a nucleotide sequence which encodes a polypeptide having at least 85% sequence identity to a polypeptide of SEQ ID NO: 2, 4, 6 or 8;

(l) a nucleotide sequence which encodes a polypeptide containing a conserved domain having at least 65% sequence identity to a conserved domain of a polypeptide of SEQ ID NO: 2, 4, 6, or 8;

(m) a nucleotide sequence which encodes a plant transcription factor comprising a fragment having 6 consecutive amino acids from a region of SEQ ID NO: 2, 4, 6, or 8 outside of the conserved domain;

(n) a nucleotide sequence having at least 85% sequence identity to (m);

(o) a nucleotide sequence which encodes a plant transcription factor comprising a fragment having 8 consecutive amino acids from a region of SEQ ID NO: 2, 4, 6, or 8 outside of the conserved domain; and

(p) a nucleotide sequence having at least 85% sequence identity to (o).

5. The isolated or recombinant polynucleotide of claim 4, further comprising a constitutive, inducible, or tissue-specific promoter operably linked to the nucleotide sequence.

6. A cloning or expression vector comprising the isolated or recombinant polynucleotide of claim 4.

7. A transformed cell comprising the vector of claim 6.

8. A transformed cell comprising the isolated or recombinant polynucleotide of claim 4.

9. An isolated or recombinant polypeptide comprising a subsequence of at least about 15 contiguous amino acids encoded by the recombinant or isolated polynucleotide of claim 4.

10. The isolated or recombinant polypeptide of claim 9, comprising a sequence selected from those of SEQ ID NO: 2, 4, 6 and 8, or a sequence comprising a conservative substitution therein.

11. A method for producing a plant having a modified biomass, the method comprising altering the expression of the isolated or recombinant polynucleotide of claim 4 or the expression levels or activity of a polypeptide of claim 9 in a plant, thereby producing a modified plant, and selecting a plant for an alteration in plant biomass.

12. The method of claim 11, wherein the plant is selected by comparing leaf area, seed yield, or fresh weight to a control or wild-type plant.

13. A method of identifying a factor that is modulated by or interacts with a polypeptide encoded by a polynucleotide of claim 4, the method comprising:
(a) expressing a polypeptide encoded by the polynucleotide in a plant; and
(b) identifying at least one factor that is modulated by or interacts with the polypeptide.

14. The method of claim 13, wherein the identifying is performed by detecting binding by the polypeptide to a promoter sequence, or detecting interactions between an additional protein and the polypeptide in a yeast two hybrid system.

15. The method of claim 13, wherein the identifying is performed by detecting expression of a factor by hybridization to a microarray, subtractive hybridization or differential display.

16. A method of identifying a molecule that modulates activity or expression of a polynucleotide or polypeptide of interest, the method comprising:
(a) placing the molecule in contact with a plant comprising the polynucleotide or polypeptide encoded by the polynucleotide of claim 4; and,
(b) monitoring one or more of: (i) expression level of the polynucleotide in the plant; (ii) expression level of the polypeptide in the plant; (iii) modulation of an activity of the polypeptide in a plant; or (iv) modulation of an activity of the polynucleotide in the plant.

17. A method of identifying a sequence homologous to one or more polynucleotides of claim 4, or one or more polypeptides encoded by the polynucleotides, the method comprising:
(a) providing a sequence database; and,
(b) querying the sequence database with one or more target sequences corresponding to the one or more polynucleotides or to the one or more polypeptides to identify one or more members of the database that display sequence similarity or homology to one or more of the target sequences.

18. The method of claim 17, wherein the querying comprises aligning one or more of the target sequences with one or more of the members of the sequence database.

19. The method of claim 17, further comprising linking the one or more polynucleotides or encoded polypeptides of claim 4 to a plant trait associated with modified plant biomass.

20. The method of claim 17, wherein the target sequence contains at least 5 consecutive amino acids of SEQ ID NO: 2, 4, 6, or 8.

21. The method of claim 17, wherein the target sequence contains at least 15 consecutive nucleotides of SEQ ID NO: 1, 3, 5, or 7.

22. A plant comprising altered expression levels of the isolated or recombinant polynucleotide of claim 4.

23. A plant comprising altered expression levels or the activity of the isolated and recombinant polypeptide of claim 9.

Figure 1

ClustalW Formatted Alignments

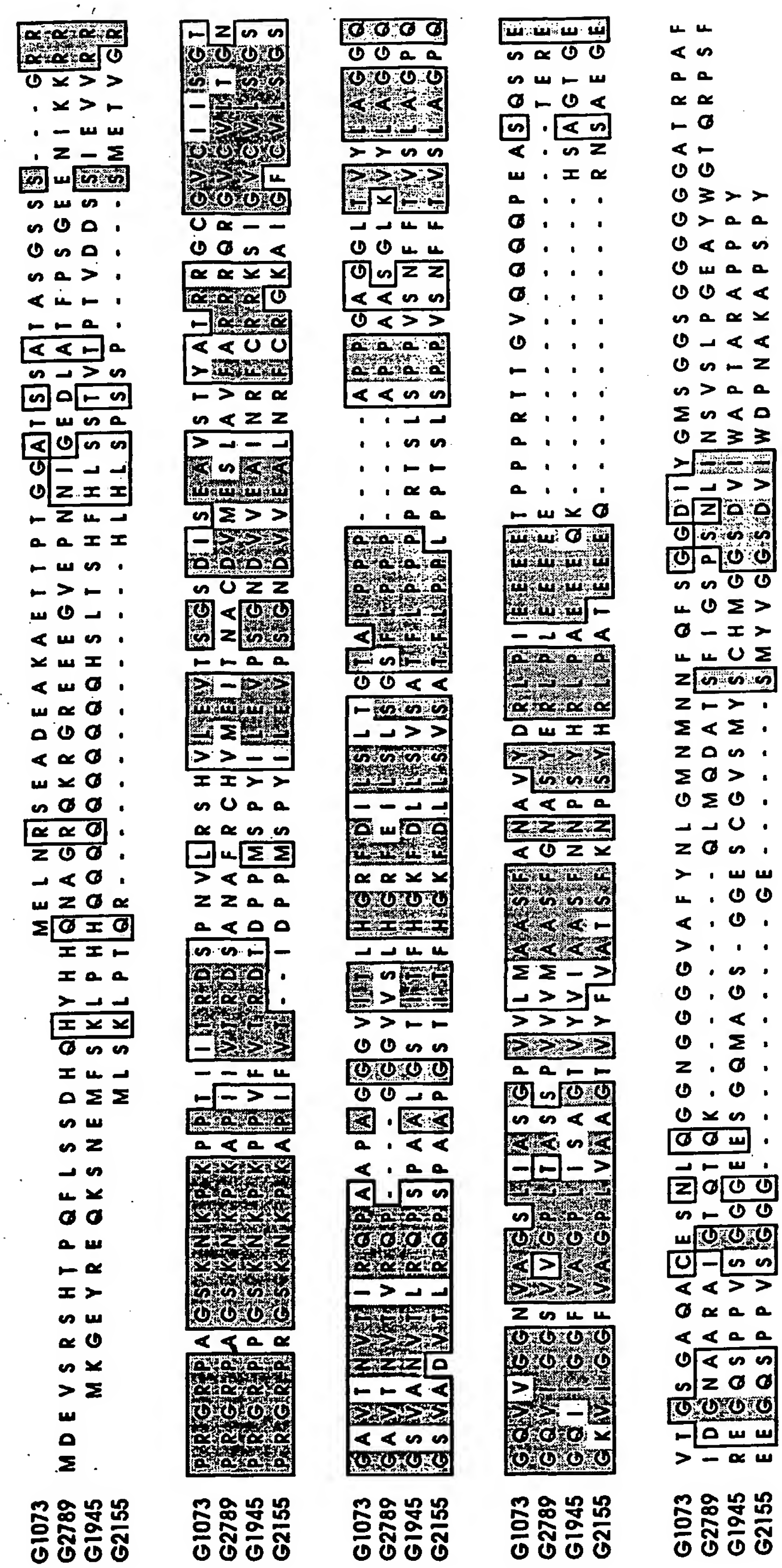
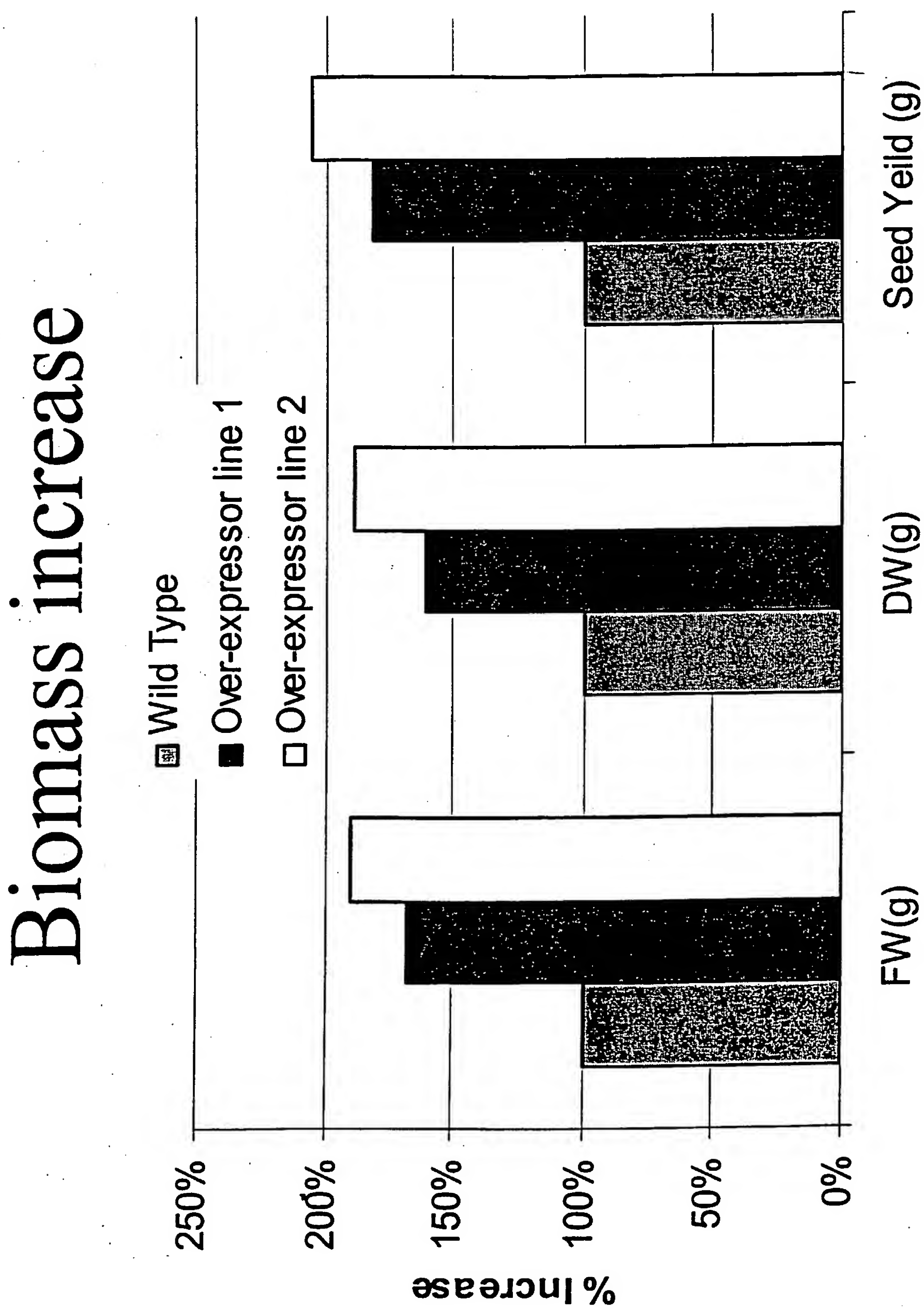


Figure 2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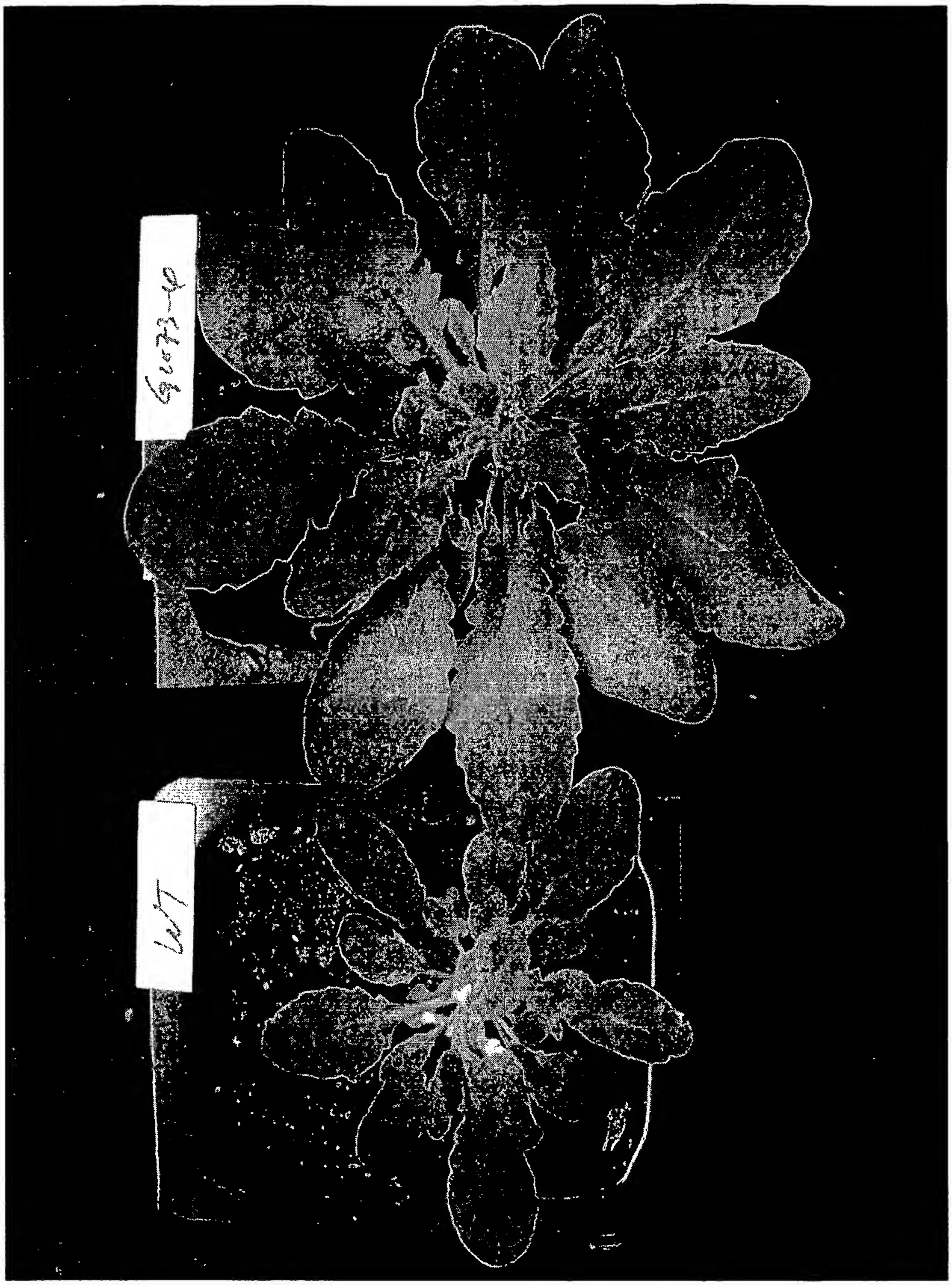
Over-expressor line 1
Over-expressor line 2
% Increase
250%
200%
150%
100%
50%
0%
FW(g)
DW(g)
Seed Yeild (g)

Figure 3

Plant overexpressing G1073 (SEQ ID NO: 1 and 2) has increased biomass compared to wild-type plant



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Ala Arg Arg Arg Gln Arg Gly Val Cys Val Leu Thr Gly Asn Gly Ala
110 115 120

gtt aca aac gtc acc gtt aga caa cct ggc gga ggc gtc gtc agt tta 495
Val Thr Asn Val Thr Val Arg Gln Pro Gly Gly Gly Val Val Ser Leu
125 130 135

cac gga cgg ttt gag att ctt tct ctc tcg ggt tcg ttt ctt cct cca 543
His Gly Arg Phe Glu Ile Leu Ser Leu Ser Gly Ser Phe Leu Pro Pro
140 145 150

ccg gca cca cca gct gcg tct ggt tta aag gtt tac tta gcc ggt ggt 591
Pro Ala Pro Pro Ala Ala Ser Gly Leu Lys Val Tyr Leu Ala Gly Gly
155 160 165 170

caa ggt caa gtg atc gga ggc agt gtg gtg gga ccg ctt acg gca tca 639
Gln Gly Gln Val Ile Gly Gly Ser Val Val Gly Pro Leu Thr Ala Ser
175 180 185

agt ccg gtg gtc gtt atg gca gct tca ttt gga aac gca tct tac gag 687
Ser Pro Val Val Val Met Ala Ala Ser Phe Gly Asn Ala Ser Tyr Glu
190 195 200

agg ctg cca cta gag gag gag gag gaa act gaa aga gaa ata gat gga 735
Arg Leu Pro Leu Glu Glu Glu Glu Glu Thr Glu Arg Glu Ile Asp Gly
205 210 215

aac gcg gct agg gcg att gga acg caa acg cag aaa cag tta atg caa 783
Asn Ala Ala Arg Ala Ile Gly Thr Gln Thr Gln Lys Gln Leu Met Gln
220 225 230

gat gcg aca tcg ttt att ggg tcg ccg tcg aat tta att aac tct gtt 831
Asp Ala Thr Ser Phe Ile Gly Ser Pro Ser Asn Leu Ile Asn Ser Val
235 240 245 250

tcg ttg cca ggt gaa gct tat tgg gga acg caa cga ccg tct ttc taa 879
Ser Leu Pro Gly Glu Ala Tyr Trp Gly Thr Gln Arg Pro Ser Phe
255 260 265

gataatatca ttgataatat aagtttcgtc ttcttattct ttttcacttt ttaccttttt 939

cactttctta ggttttgttt taacgtttga ttaatacctg aaggtttttg gaaaattttc 999

gatcggataa aaggatttat gttgcgagcc gaaacgcggc c 1040

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<213> Arabidopsis thaliana

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Met Asp Glu Val Ser Arg Ser His Thr Pro Gln Phe Leu Ser Ser Asp
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His Gln His Tyr His His Gln Asn Ala Gly Arg Gln Lys Arg Gly Arg
20 25 30

Glu Glu Glu Gly Val Glu Pro Asn Asn Ile Gly Glu Asp Leu Ala Thr
        35   40   45

Phe Pro Ser Gly Glu Glu Asn Ile Lys Lys Arg Arg Pro Arg Gly Arg
    50   55   60

Pro Ala Gly Ser Lys Asn Lys Pro Lys Ala Pro Ile Ile Val Thr Arg
65   70   75   80

Asp Ser Ala Asn Ala Phe Arg Cys His Val Met Glu Ile Thr Asn Ala
                85   90   95

Cys Asp Val Met Glu Ser Leu Ala Val Phe Ala Arg Arg Arg Gln Arg
            100   105   110

Gly Val Cys Val Leu Thr Gly Asn Gly Ala Val Thr Asn Val Thr Val
        115   120   125

Arg Gln Pro Gly Gly Gly Val Val Ser Leu His Gly Arg Phe Glu Ile
    130   135   140

Leu Ser Leu Ser Gly Ser Phe Leu Pro Pro Pro Ala Pro Pro Ala Ala
145   150   155   160

Ser Gly Leu Lys Val Tyr Leu Ala Gly Gly Gln Gly Gln Val Ile Gly
                165   170   175

Gly Ser Val Val Gly Pro Leu Thr Ala Ser Ser Pro Val Val Val Met
            180   185   190

Ala Ala Ser Phe Gly Asn Ala Ser Tyr Glu Arg Leu Pro Leu Glu Glu
        195   200   205

Glu Glu Glu Thr Glu Arg Glu Ile Asp Gly Asn Ala Ala Arg Ala Ile
    210   215   220

Gly Thr Gln Thr Gln Lys Gln Leu Met Gln Asp Ala Thr Ser Phe Ile
225   230   235   240

Gly Ser Pro Ser Asn Leu Ile Asn Ser Val Ser Leu Pro Gly Glu Ala
                245   250   255

Tyr Trp Gly Thr Gln Arg Pro Ser Phe
            260   265

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<223> G1945

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ccaacaacct ctacatcttc ttcttcttct tcctcctctt ttattttctt tttaaatcat     120

ttacacaaaa atccaaagac aaatctgaaa tctctaataa acaaatccat aaaataagaa     180

aaacaaag atg aaa ggt gaa tac aga gag caa aag agt aac gaa atg ttt      230
         Met Lys Gly Glu Tyr Arg Glu Gln Lys Ser Asn Glu Met Phe
         1               5                   10

tcc aag ctt cct cat cat caa caa caa cag caa caa caa caa caa caa      278
Ser Lys Leu Pro His His Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
15                  20                  25                  30

cac tct ctt acc tct cac ttc cac ctc tcc tcc acc gta acc ccc acc      326
His Ser Leu Thr Ser His Phe His Leu Ser Ser Thr Val Thr Pro Thr
                35                  40                  45

gtc gat gac tcc tcc atc gaa gtg gtc cga cgt cca cgt ggc aga cca      374
Val Asp Asp Ser Ser Ile Glu Val Val Arg Arg Pro Arg Gly Arg Pro
            50                  55                  60

cca ggt tcc aaa aac aaa cct aaa cca ccc gtc ttc gtc aca cgt gac      422
Pro Gly Ser Lys Asn Lys Pro Lys Pro Pro Val Phe Val Thr Arg Asp
        65                  70                  75

acc gac cct cct atg agt cct tac atc ctc gaa gtt cct tca gga aac      470
Thr Asp Pro Pro Met Ser Pro Tyr Ile Leu Glu Val Pro Ser Gly Asn
    80                  85                  90

gac gtc gtc gaa gcc atc aac cgt ttc tgc cgc cgt aaa tcc atc gga      518
Asp Val Val Glu Ala Ile Asn Arg Phe Cys Arg Arg Lys Ser Ile Gly
95                  100                 105                 110

gtc tgc gtc ctt agt ggc tct ggc tct gta gct aac gtc act tta cgt      566
Val Cys Val Leu Ser Gly Ser Gly Ser Val Ala Asn Val Thr Leu Arg
                115                 120                 125

cag cca tca ccg gca gct ctt ggc tct acc ata act ttc cat gga aag      614
Gln Pro Ser Pro Ala Ala Leu Gly Ser Thr Ile Thr Phe His Gly Lys
            130                 135                 140

ttt gat ctc ctc tcc gtc tcc gca acg ttt ctc cct cct ccg cct cgt      662
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Phe Asp Leu Leu Ser Val Ser Ala Thr Phe Leu Pro Pro Pro Pro Arg
        145                 150                 155

act tcc ttg tct cct ccc gtt tct aac ttc ttc acc gtc tct ctc gct       710
Thr Ser Leu Ser Pro Pro Val Ser Asn Phe Phe Thr Val Ser Leu Ala
    160                 165                 170

gga cct caa gga caa atc atc gga ggg ttc gtc gct ggt cca ctt att       758
Gly Pro Gln Gly Gln Ile Ile Gly Gly Phe Val Ala Gly Pro Leu Ile
175                 180                 185                 190

tcg gca gga aca gtt tac gtc atc gcc gca agt ttc aac aac cct tct       806
Ser Ala Gly Thr Val Tyr Val Ile Ala Ala Ser Phe Asn Asn Pro Ser
                195                 200                 205

tat cac cgg tta ccg gcg gaa gaa gag caa aaa cac tcg gcg ggg aca       854
Tyr His Arg Leu Pro Ala Glu Glu Glu Gln Lys His Ser Ala Gly Thr
            210                 215                 220

ggg gaa aga gag gga caa tct ccg ccg gtc tct ggt ggc ggt gaa gag       902
Gly Glu Arg Glu Gly Gln Ser Pro Pro Val Ser Gly Gly Gly Glu Glu
        225                 230                 235

tca gga cag atg gcg gga agt gga gga gag tcg tgt ggg gta tca atg       950
Ser Gly Gln Met Ala Gly Ser Gly Gly Glu Ser Cys Gly Val Ser Met
    240                 245                 250

tac agt tgc cac atg ggt ggc tct gat gtt att tgg gcc cct aca gcc       998
Tyr Ser Cys His Met Gly Gly Ser Asp Val Ile Trp Ala Pro Thr Ala
255                 260                 265                 270

aga gct cca ccg cca tac taa ccaatccttc tttcacaaat ctctttcttt         1049
Arg Ala Pro Pro Pro Tyr
                275

ctttttttgt tttttttgt tttgggttag gatgaatcaa gaaactaggg ttttttttt    1109

ttttttttaa aaaaaaaaaa a                                              1130

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<212>  PRT

<213>  Arabidopsis thaliana


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Met Lys Gly Glu Tyr Arg Glu Gln Lys Ser Asn Glu Met Phe Ser Lys
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Leu Pro His His Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln His Ser
            20                  25                  30


Leu Thr Ser His Phe His Leu Ser Ser Thr Val Thr Pro Thr Val Asp
        35                  40                  45
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Asp Ser Ser Ile Glu Val Val Arg Arg Pro Arg Gly Arg Pro Pro Gly
50 55 60

Ser Lys Asn Lys Pro Lys Pro Pro Val Phe Val Thr Arg Asp Thr Asp
65 70 75 80

Pro Pro Met Ser Pro Tyr Ile Leu Glu Val Pro Ser Gly Asn Asp Val
85 90 95

Val Glu Ala Ile Asn Arg Phe Cys Arg Arg Lys Ser Ile Gly Val Cys
100 105 110

Val Leu Ser Gly Ser Gly Ser Val Ala Asn Val Thr Leu Arg Gln Pro
115 120 125

Ser Pro Ala Ala Leu Gly Ser Thr Ile Thr Phe His Gly Lys Phe Asp
130 135 140

Leu Leu Ser Val Ser Ala Thr Phe Leu Pro Pro Pro Pro Arg Thr Ser
145 150 155 160

Leu Ser Pro Pro Val Ser Asn Phe Phe Thr Val Ser Leu Ala Gly Pro
165 170 175

Gln Gly Gln Ile Ile Gly Gly Phe Val Ala Gly Pro Leu Ile Ser Ala
180 185 190

Gly Thr Val Tyr Val Ile Ala Ala Ser Phe Asn Asn Pro Ser Tyr His
195 200 205

Arg Leu Pro Ala Glu Glu Glu Gln Lys His Ser Ala Gly Thr Gly Glu
210 215 220

Arg Glu Gly Gln Ser Pro Pro Val Ser Gly Gly Gly Glu Glu Ser Gly
225 230 235 240

Gln Met Ala Gly Ser Gly Gly Glu Ser Cys Gly Val Ser Met Tyr Ser
245 250 255

Cys His Met Gly Gly Ser Asp Val Ile Trp Ala Pro Thr Ala Arg Ala
260 265 270

Pro Pro Pro Tyr
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<222> (63)..(740)

<223> G2155

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Met Leu Ser Lys Leu Pro Thr Gln Arg His Leu His Leu Ser Pro
1 5 10 15

tcc tct ccc tcc atg gaa acc gtc ggg cgt cca cgt ggc aga cct cga 155
Ser Ser Pro Ser Met Glu Thr Val Gly Arg Pro Arg Gly Arg Pro Arg
20 25 30

ggt tcc aaa aac aaa cct aaa gct cca atc ttt gtc acc att gac cct 203
Gly Ser Lys Asn Lys Pro Lys Ala Pro Ile Phe Val Thr Ile Asp Pro
35 40 45

cct atg agt cct tac atc ctc gaa gtg cca tcc gga aac gat gtc gtt 251
Pro Met Ser Pro Tyr Ile Leu Glu Val Pro Ser Gly Asn Asp Val Val
50 55 60

gaa gcc cta aac cgt ttc tgc cgc ggt aaa gcc atc ggc ttt tgc gtc 299
Glu Ala Leu Asn Arg Phe Cys Arg Gly Lys Ala Ile Gly Phe Cys Val
65 70 75

ctc agt ggc tca ggc tcc gtt gct gat gtc act ttg cgt cag cct tct 347
Leu Ser Gly Ser Gly Ser Val Ala Asp Val Thr Leu Arg Gln Pro Ser
80 85 90 95

ccg gca gct cct ggc tca acc att act ttc cac gga aag ttc gat ctt 395
Pro Ala Ala Pro Gly Ser Thr Ile Thr Phe His Gly Lys Phe Asp Leu
100 105 110

ctc tct gtc tcc gcc act ttc ctc cct cct cta cct cct acc tcc ttg 443
Leu Ser Val Ser Ala Thr Phe Leu Pro Pro Leu Pro Pro Thr Ser Leu
115 120 125

tcc cct ccc gtc tcc aat ttc ttc acc gtc tct ctc gcc gga cct cag 491
Ser Pro Pro Val Ser Asn Phe Phe Thr Val Ser Leu Ala Gly Pro Gln
130 135 140

ggg aaa gtc atc ggt gga ttc gtc gct ggt cct ctc gtt gcc gcc gga 539
Gly Lys Val Ile Gly Gly Phe Val Ala Gly Pro Leu Val Ala Ala Gly
145 150 155

act gtt tac ttc gtc gcc act agt ttc aag aac cct tcc tat cac cgg 587
Thr Val Tyr Phe Val Ala Thr Ser Phe Lys Asn Pro Ser Tyr His Arg
160 165 170 175

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tta cct gct acg gag gaa gag caa aga aac tcg gcg gaa ggg gaa gag      635
Leu Pro Ala Thr Glu Glu Glu Gln Arg Asn Ser Ala Glu Gly Glu Glu
                180                 185                 190

gag gga caa tcg ccg ccg gtc tct gga ggt ggt gga gag tcg atg tac      683
Glu Gly Gln Ser Pro Pro Val Ser Gly Gly Gly Gly Glu Ser Met Tyr
            195                 200                 205

gtg ggt ggc tct gat gtc att tgg gat ccc aac gcc aaa gct cca tcg      731
Val Gly Gly Ser Asp Val Ile Trp Asp Pro Asn Ala Lys Ala Pro Ser
        210                 215                 220

ccg tac tga ccacaaatcc atctcgttca aactagggtt tcttcttctt             780
Pro Tyr
    225

tagatcatca agaatcaaca aaaagattgc atttttagat tctttgtaat atcataattg   840

actcactctt taatctctct atcacttctt ctttagcttt ttctgcagtg tcaaacttca   900

catatttgta gtttgatttg actatcccca agttttgtat tttatcatac aaatttttgc   960

ctgtctctaa tggttgtttt ttcgtttgta taatcttatg cattgtttat tggagctcca  1020

gagattgaat gtataatata atggtttaat                                   1050
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<212> PRT

<213> Arabidopsis thaliana

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            20                  25                  30

Ser Lys Asn Lys Pro Lys Ala Pro Ile Phe Val Thr Ile Asp Pro Pro
        35                  40                  45

Met Ser Pro Tyr Ile Leu Glu Val Pro Ser Gly Asn Asp Val Val Glu
    50                  55                  60

Ala Leu Asn Arg Phe Cys Arg Gly Lys Ala Ile Gly Phe Cys Val Leu
65                  70                  75                  80

Ser Gly Ser Gly Ser Val Ala Asp Val Thr Leu Arg Gln Pro Ser Pro
                85                  90                  95
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Ala Ala Pro Gly Ser Thr Ile Thr Phe His Gly Lys Phe Asp Leu Leu
            100   105   110

Ser Val Ser Ala Thr Phe Leu Pro Pro Leu Pro Pro Thr Ser Leu Ser
        115   120   125

Pro Pro Val Ser Asn Phe Phe Thr Val Ser Leu Ala Gly Pro Gln Gly
    130   135   140

Lys Val Ile Gly Gly Phe Val Ala Gly Pro Leu Val Ala Ala Gly Thr
145   150   155   160

Val Tyr Phe Val Ala Thr Ser Phe Lys Asn Pro Ser Tyr His Arg Leu
                165   170   175

Pro Ala Thr Glu Glu Glu Gln Arg Asn Ser Ala Glu Gly Glu Glu Glu
            180   185   190

Gly Gln Ser Pro Pro Val Ser Gly Gly Gly Gly Glu Ser Met Tyr Val
        195   200   205

Gly Gly Ser Asp Val Ile Trp Asp Pro Asn Ala Lys Ala Pro Ser Pro
    210   215   220

Tyr
225